



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 158189

TO: Ruixiang Li
Location: rem/4D75/4C70
Art Unit: 1646
Monday, July 11, 2005
Case Serial Number: 10/060765

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

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From: Li, Ruixiang
Sent: Tuesday, July 05, 2005 11:55 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/060,765

Please do a standard search on:

- (i). SEQ ID NOS: 4, 7, and 8 against both commercial and interference amino acid databases.
(ii). An oligomer of SEQ ID NO: 4 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

Claim 15. An epitope-bearing portion of the polypeptide of SEQ ID NO: 4.

Claim 16. The epitope-bearing portion of claim 15, which comprises between 10 and 50 contiguous amino acids of SEQ ID NO: 4.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:40:07 ; Search time 42 Seconds
(without alignments)
371.468 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 209
Sequence: 1 MDSDETFEHSGLVWSVLG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table:  Gapop 60.0, Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	209	4	US-09-715-805-4
2	173	82.8	209	4	US-09-390-207-2
3	145	69.4	181	4	US-09-390-207-5
4	79	37.8	85	4	US-09-621-976-5213
5	30	14.4	181	4	US-09-390-207-6
6	30	14.4	210	4	US-09-390-207-4
7	30	14.4	210	4	US-09-715-805-2
8	28	13.4	28	4	US-09-390-207-41
9	16	7.7	16	4	US-09-715-805-7
10	15	7.2	15	4	US-09-715-805-8
11	8	3.8	477	4	US-09-252-991A-19831
12	8	3.8	564	4	US-09-902-540-16018
13	7	3.3	15	3	US-08-602-999A-394
14	7	3.3	15	4	US-09-009-953-10
15	7	3.3	15	4	US-09-009-953-11
16	7	3.3	15	4	US-09-009-953-42
17	7	3.3	15	4	US-09-009-953-43
18	7	3.3	15	4	US-09-500-124-394
19	7	3.3	15	4	US-09-311-784A-415
20	7	3.3	19	1	US-07-908-317-7
21	7	3.3	19	5	PCT-US93-06171-7
22	7	3.3	90	4	US-08-311-731A-356
23	7	3.3	103	4	US-09-252-991A-28978
24	7	3.3	143	4	US-09-621-976-7099
25	7	3.3	150	4	US-09-328-352-6423
26	7	3.3	162	2	US-08-313-704-6
27	7	3.3	221	4	US-09-489-039A-8256

ALIGNMENTS

RESULT 1

US-09-715-805-4
; Sequence 4, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626yuyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715.805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-4

Query Match 100.0%; Score 209; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.1e-193;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDSDETFEHSGLVWSVLGALLGACQAHPTPDSPLQFGQVQRXYLYTDDAQQTSAH	60
Db	1	MDSDETFEHSGLVWSVLGALLGACQAHPTPDSPLQFGQVQRXYLYTDDAQQTSAH	60
Qy	61	LEIRDEGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCORPDGALVGSLLHFDPEA	120
Db	61	LEIRDEGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCORPDGALVGSLLHFDPEA	120
Qy	121	CSFRELLEDGYNVYQSEAHGLPLHLFGNKSPPHRDPAPRGPARFLPLGLPPALPEPPGI	180
Db	121	CSFRELLEDGYNVYQSEAHGLPLHLFGNKSPPHRDPAPRGPARFLPLGLPPALPEPPGI	180
Qy	181	LAPOPPDVGSSDPLSMVGPQGRSPSYAS	209
Db	181	LAPOPPDVGSSDPLSMVGPQGRSPSYAS	209

RESULT 2

US-09-390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomson, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371

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; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match      82.8%; Score 173; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1e-158;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFGHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFGHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60

QY 61 LEIRDGTGGAADQSPESLLQLKALPGVQILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIRDGTGGAADQSPESLLQLKALPGVQILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPA 173
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPA 173

RESULT 3
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match      69.4%; Score 145; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 8.6e-132;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 HPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAHLEIRDGTGGAADQSPESLLQLKALKP 88
DB 1 HPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAHLEIRDGTGGAADQSPESLLQLKALKP 60

QY 89 GVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEACSFRELLEDGYNVYQSEAHGLPLHLPG 148
DB 61 GVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEACSFRELLEDGYNVYQSEAHGLPLHLPG 120

QY 149 NKSPhRDPA PRGPAPRFLPLGLPPA 173
DB 121 NKSPhRDPA PRGPAPRFLPLGLPPA 145

RESULT 4
US-09-621-976-5213
; Sequence 5213, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
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; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-5213

Query Match      37.8%; Score 79; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.7e-68;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFGHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFGHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60

QY 61 LEIRDGTGGAADQSPES 79
DB 61 LEIRDGTGGAADQSPES 79

RESULT 5
US-09-390-207-6
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6

Query Match      14.4%; Score 30; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 HFDPEACSFRELLEDGYNVYQSEAHGLPL 144
DB 87 HFDPEACSFRELLEDGYNVYQSEAHGLPL 116

RESULT 6
US-09-390-207-4
; Sequence 4, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 4
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-4

Query Match
Best Local Similarity 14.4%; Score 30; DB 4; Length 210;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 144
      |||||
DB 116 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 145
      |||||

RESULT 7
US-09-715-805-2
; Sequence 2, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-715-805-2

Query Match
Best Local Similarity 14.4%; Score 30; DB 4; Length 210;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 144
      |||||
DB 116 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 145
      |||||

RESULT 8
US-09-390-207-41
; Sequence 41, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-41

Query Match
Best Local Similarity 13.4%; Score 28; DB 4; Length 28;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFGEHSGLWVSVLAGLLIGACQA 28
      |||||
DB 1 MDSDETFGEHSGLWVSVLAGLLIGACQA 28
      |||||

RESULT 9
US-09-715-805-7
; Sequence 7, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-7

Query Match
Best Local Similarity 7.7%; Score 16; DB 4; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 RQRYLYTDDAQOQTEAH 60
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DB 1 RQRYLYTDDAQOQTEAH 16
      |||||

RESULT 10
US-09-715-805-8
; Sequence 8, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-8

Query Match
Best Local Similarity 7.2%; Score 15; DB 4; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 HLPGNKSPHRDPAPR 159
      |||||
DB 1 HLPGNKSPHRDPAPR 15
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RESULT 11
US-09-252-991A-19831
; Sequence 19831, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 19831
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19831

Query Match          3.8%; Score 8; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 DPAPRGPA 162
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Db 155 DPAPRGPA 162

RESULT 12
US-09-902-540-16018
; Sequence 16018, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16018
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16018

Query Match          3.8%; Score 8; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLAGLLLG 24
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Db 483 VLAGLLLG 490

RESULT 13
US-08-602-999A-394
; Sequence 394, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 394:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-394

Query Match          3.3%; Score 7; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LPGLPPA 173
    |||||
Db 7 LPGLPPA 13

RESULT 14
US-09-009-953-10
; Sequence 10, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-009-953-10

Query Match 3.3%; Score 7; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVLAGLL 22
Db 9 SVLAGLL 15

RESULT 15
US-09-009-953-11
; Sequence 11, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-009-953-11

Query Match 3.3%; Score 7; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVLAGLL 22
Db 7 SVLAGLL 13

Search completed: July 8, 2005, 22:52:20
Job time : 44 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 22:38:19 ; Search time 40 Seconds
(without alignments)
502.733 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 209
Sequence: 1 MDSDTGFHSLWVSLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table:  Gap 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79.*

1: Piri.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.8	568	2 E75502	threonine ammonia-
2	8	3.8	584	2 H71513	probable ssdna exo
3	8	3.8	666	2 T22943	hypothetical prote
4	7	3.3	90	2 C73345	hypothetical prote
5	7	3.3	92	2 S21307	hypothetical prote
6	7	3.3	120	2 T18135	hypothetical prote
7	7	3.3	121	2 I35719	phnQ protein - Bac
8	7	3.3	146	2 H75394	conserved hypothet
9	7	3.3	157	2 F83242	hypothetical prote
10	7	3.3	162	1 YACQ51	antigen 5.1 precu
11	7	3.3	162	2 A25780	blood-stage antige
12	7	3.3	162	2 A26769	antigen 5.1 precu
13	7	3.3	163	2 F72565	hypothetical prote
14	7	3.3	208	2 A83682	urase accessory p
15	7	3.3	219	2 S14242	yopE protein - Yec
16	7	3.3	248	2 F75200	hypothetical prote
17	7	3.3	250	2 F83609	hypothetical prote
18	7	3.3	257	2 E90763	hypothetical prote
19	7	3.3	257	2 F85626	hypothetical prote
20	7	3.3	262	2 AB2488	hypothetical prote
21	7	3.3	288	2 T37029	hypothetical prote
22	7	3.3	295	2 S60768	GTP-binding protei
23	7	3.3	302	2 H82638	hypothetical prote
24	7	3.3	330	2 D95963	probable phosphat
25	7	3.3	330	2 AG2129	iron(III) dicitrat
26	7	3.3	332	2 A95404	probable ABC trans
27	7	3.3	340	2 E83126	ferric enterobacti
28	7	3.3	347	2 B87274	hypothetical prote
29	7	3.3	349	2 A10274	L-arabinose transp

30	7	3.3	376	2 B41870	DNA-directed DNA p
31	7	3.3	388	2 A45304	granulocyte/macrop
32	7	3.3	389	1 C69092	conserved hypothet
33	7	3.3	402	2 A70882	probable pPE prote
34	7	3.3	410	2 T50718	hypothetical prote
35	7	3.3	421	2 T43534	transcription fact
36	7	3.3	431	2 S09824	hypothetical prote
37	7	3.3	442	2 D72498	probable serine hy
38	7	3.3	446	2 D98811	hypothetical prote
39	7	3.3	467	2 F86837	transcription regu
40	7	3.3	469	2 D84454	hypothetical prote
41	7	3.3	471	2 D83388	probable MFS trans
42	7	3.3	476	2 A84454	hypothetical prote
43	7	3.3	476	2 B84454	hypothetical prote
44	7	3.3	476	2 C84454	hypothetical prote
45	7	3.3	477	2 S77373	hypothetical prote

ALIGNMENTS

RESULT 1

E75502

Threonine ammonia-lyase (EC 4.3.1.19) DR0567 [similarity] - Deinococcus radiodurans (str

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: E75502

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75502

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-568 <WHI>

A:Cross-references: UNIPROT:Q9RWU8; GB:AE001915; GB:AE005513; NID:G6458262; PIDN:AAF1014

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0567

A:Map position: 1

C:Superfamily: threonine dehydratase

C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos

F:116/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 3.8%; Score 8; DB 2; Length 568;

Best Local Similarity 100.0%; Pred. No. 8.4; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0;

QY 83 LKALKPGV 90

DB 255 LKALKPGV 262

RESULT 2

H71513

probable ssdna exonuclease - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: H71513

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: H71513

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <ARN>

A:Cross-references: UNIPROT:O84453; GB:AE001318; GB:AE001273; NID:G3328875; PIDN:AAC6804

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: recJ

C;Superfamily: single-stranded-DNA-specific exonuclease RecJ

Query Match 3.8%; Score 8; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 QILGVKTS 99
|||||
DB 110 QILGVKTS 117

RESULT 3

T22943

hypothetical protein F58G11.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22943

R;Percy, C.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19640

A;Accession: T22943

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-666 <WIL>

A;Cross-references: UNIPROT:P90898; EMBL:Z81094; PIDN:CAB03154.1; GSPDB:GN00023; CESP:F5

A;Experimental source: clone F58G11

C;Genetics:

A;Gene: CESP:F58G11.3

A;Map position: 5

A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3

Query Match

Best Local Similarity 100.0%; Pred. No. 9.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LIQLKALK 87

|||||

DB 470 LIQLKALK 477

RESULT 4

C75345

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: C75345

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999.

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75345

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-90 <WHL>

A;Cross-references: UNIPROT:Q9RTB8; GB:AE002025; GB:AE000513; NID:G6459627; PIDN:AAF1140

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR1847

A;Map position: 1

Query Match

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLGLLL 23

|||||

DB 24 VLGLLL 30

RESULT 5

S21307

hypothetical protein - Pseudomonas aeruginosa

C;Species: Pseudomonas aeruginosa

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S21307

R;Davies, S.S.P.; Krishnapillai, V.V.

submitted to the EMBL Data Library, September 1990

A;Description: DNA sequence analysis of the replication region of the Pseudomonas aerugi

A;Reference number: S21306

A;Accession: S21307

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-92 <DAV>

A;Cross-references: UNIPROT:Q51557; EMBL:X54695; NID:G45410; PIDN:CAA38511.1; PID:G45412

Query Match 3.3%; Score 7; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SSPLLQF 40

|||||

DB 74 SSPLLQF 80

RESULT 6

T18135

hypothetical protein A633R - Chlorella virus PBCV-1

C;Species: Chlorella virus PBCV-1

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18135

R;Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A;Reference number: Z18806

A;Accession: T18135

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-120 <GRA>

A;Cross-references: UNIPROT:O41115; EMBL:U42580; NID:G4028896; PIDN:AAC96960.1

A;Experimental source: specific host Chlorella strain NC64A

C;Genetics:

A;Note: A633R

C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A633R

Query Match

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LAGLLLG 24

|||||

DB 15 LAGLLLG 21

RESULT 7

I35719

phnQ protein - Escherichia coli

C;Species: Escherichia coli

C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004

C;Accession: I35719

R;Chen, C.M.; Ye, Q.Z.; Zhu, Z.; Wanner, B.L.; Walsh, C.T.

J. Biol. Chem. 265, 4461-4471, 1990

A;Title: Molecular biology of carbon-phosphorus bond cleavage. Cloning and sequencing of

A;Reference number: A35718; MUID:90170953; PMID:2155230

A;Accession: I35719

A;Molecule type: DNA

A;Residues: 1-121 <CHE>

A;Cross-references: UNIPROT:P16693; GB:J05260; NID:G147192; PIDN:AAA24357.1; PID:G147214

Query Match 3.3%; Score 7; DB 2; Length 121;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ARFLPLP 168

|||||

DB 39 ARFLPLP 45

RESULT 8

H75394 conserved hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: H75394
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: H75394
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <WHI>
 A:CROSS-references: UNIPROT:Q9RUD7; GB:AE001989; GB:AE000513; NID:G6459202; PIDN:AAF1101
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1450
 A:Map position: 1

Query Match 3.3%; Score 7; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AGLLIGA 25
 |||||
 DB 115 AGLLIGA 121

RESULT 9

F83242 hypothetical protein PA3218 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: F83242
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: F83242
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <STO>
 A:CROSS-references: UNIPROT:Q9H222; GB:AE004745; GB:AE004091; NID:G9949336; PIDN:AAG0660
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3218

Query Match 3.3%; Score 7; DB 2; Length 157;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 PAPRGPA 162
 |||||
 DB 79 PAPRGPA 85

RESULT 10

YAZ051 antigen 5.1 precursor - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C:Accession: A23052
 R:Hope, I.A.; Mackay, M.; Hyde, J.E.; Goman, M.; Scaife, J.
 Nucleic Acids Res. 13, 369-379, 1985
 A>Title: The gene for an exported antigen of the malaria parasite Plasmodium falciparum
 A:Reference number: A23052; MUID:85215483; PMID:2582354

A:Accession: A23052
 A:Molecule type: mRNA
 A:Residues: 1-162 <HOP>

A:CROSS-references: UNIPROT:P04926; GB:X01745; NID:G9858; PIDN:CAA25881.1; PID:G758218
 C:Comment: This antigen may be secreted by the intraerythrocyte stage into the cytoplasm of the host erythrocyte.
 C:Comment: This antigen and the circumsporozoite protein appear to have a common epitope
 C:Superfamily: plasmodium S-antigen
 C:Keywords: sporozoite; surface antigen; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-162/Product: antigen 5.1 #status predicted <MAT>
 F:76-101/Domain: transmembrane #status predicted <TM>

Query Match 3.3%; Score 7; DB 1; Length 162;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVLAGLL 22
 |||||
 DB 79 SVLAGLL 85

RESULT 11

A25780 blood-stage antigen precursor - malaria parasite (Plasmodium falciparum)
 N:Alternate names: exp-1/CRA; vacuole membrane antigen QF116
 C:Species: Plasmodium falciparum
 C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
 C:Accession: A25780; A60658
 R:Coppel, R.L.; Favaloro, J.M.; Crewther, P.E.; Burkot, T.R.; Bianco, A.E.; Stahl, H.D.; Proc. Natl. Acad. Sci. U.S.A. 82, 5121-5125, 1985
 A>Title: A blood stage antigen of Plasmodium falciparum shares determinants with the sporozoite vacuole membrane antigen QF116
 A:Reference number: A25780; MUID:85270476; PMID:2410913
 A:Accession: A25780
 A:Molecule type: mRNA
 A:Residues: 1-162 <COP>
 A:CROSS-references: UNIPROT:P04923; GB:M1145; NID:G160158; PIDN:AA29523.1; PID:G160159
 R:Kara, U.; Murray, B.; Pam, C.; Lahnstein, J.; Gould, H.; Kidson, C.; Saul, A.
 Mol. Biochem. Parasitol. 38, 19-24, 1990
 A>Title: Chemical characterization of the parasitophorous vacuole membrane antigen QF 11
 A:Reference number: A60658; MUID:90205955; PMID:1690855
 A:Accession: A60658

A:Molecule type: protein
 A:Residues: 23-40 <KAR>
 C:Comment: This vacuolar body binding not to be truncated at the carboxyl terminus.
 C:Superfamily: plasmodium S-antigen
 C:Keywords: membrane protein; myristylation; surface antigen
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-162/Product: blood-stage antigen #status experimental <MAT>

Query Match 3.3%; Score 7; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVLAGLL 22
 |||||
 DB 79 SVLAGLL 85

RESULT 12

A26769 antigen 5.1 precursor - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 19-Nov-1988 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A26769
 R:Simmons, D.; Woollett, G.; Bergin-Cartwright, M.; Kay, D.; Scaife, J.
 EMBO J. 6, 485-491, 1987
 A>Title: A malaria protein exported into a new compartment within the host erythrocyte.
 A:Reference number: A26769; MUID:87218504; PMID:2438130
 A:Accession: A26769
 A:Molecule type: DNA
 A:Residues: 1-162 <SIM>

A;Cross-references: UNIPROT:P04926; GB:X05074; NID:99890; PIDN:CAA28735.1; PID:g9891
A;Note: the authors translated the codon GTT for residue 10 as Ala
C;Superfamily: plasmodium S-antigen
C;Keywords: transmembrane protein

Query Match 3.3%; Score 7; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 SVLAGLL 22
Db 79 SVLAGLL 85
|||||

RESULT 13
F72565
hypothetical protein APE1808 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72565
R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72565
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <KAW>
A;Cross-references: UNIPROT:Q9YAY7; DDBJ:AP000062; NID:g5105244; PIDN:BAA80811.1; PID:dl
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1808
C;Superfamily: Aeropyrum pernix hypothetical protein APE1808

Query Match 3.3%; Score 7; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AGLLIGA 25
Db 65 AGLLIGA 71
|||||

RESULT 14
A83682
urease accessory protein ureG [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83682
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; HiraNucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: UNIPROT:Q9KG56; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA8039
A;Experimental source: strain C-125
C;Genetics:
A;Gene: ureG
C;Superfamily: Ni2+-binding GTPase ([NiFe]-hydrogenase/urease maturation factor)

Query Match 3.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 RELLED 130
Db 195 RELLED 201
|||||

RESULT 15

S14242

YopE protein - Yersinia enterocolitica virulence plasmid pYVe439-80

C;Species: Yersinia enterocolitica

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S14242

R;Michiels, T.; Wattiau, P.; Brasseur, R.; Ruysschaert, J.M.; Cornelis, G.

Infect. Immun. 58, 2840-2849, 1990

A;Title: Secretion of Yop proteins by Yersinia.

A;Reference number: S14239; MUID:90354044; PMID:2129533

A;Accession: S14242

A;Molecule type: DNA

A;Residues: 1-219 <MIC>

A;Cross-references: UNIPROT:P31492; EMBL:M92066; NID:g155528; PIDN:AA19862.1; PID:g1555

A;Experimental source: strain W22703 serotype O:9

C;Genetics:

A;Gene: yopE; yop25

A;Genome: plasmid pYVe439-80

Query Match 3.3%; Score 7; DB 2; Length 219;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 GTVGGAA 73

Db 182 GTVGGAA 188

|||||

Search completed: July 8, 2005, 22:51:31

Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:50:52 ; Search time 164 Seconds
(without alignments)
492.336 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 209
Sequence: 1 MDSDETFEHSGLVWVSLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1726216 seqs, 386330316 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCT05_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	209	9 US-09-822-485-24	Sequence 24, Appl
2	209	100.0	209	9 US-09-801-968-15	Sequence 15, Appl
3	209	100.0	209	10 US-09-802-154-15	Sequence 15, Appl
4	209	100.0	209	13 US-10-060-765-4	Sequence 4, Appl
5	209	100.0	209	14 US-10-374-207-24	Sequence 24, Appl
6	209	100.0	209	16 US-10-818-140-4	Sequence 4, Appl
7	209	100.0	209	17 US-10-771-173-4	Sequence 4, Appl
8	203	97.1	209	17 US-10-659-004-68	Sequence 68, Appl
9	203	97.1	209	17 US-10-659-004-70	Sequence 70, Appl
10	192	91.9	209	17 US-10-659-004-66	Sequence 66, Appl
11	188	90.0	208	9 US-09-755-695-2	Sequence 2, Appl

12	188	90.0	208	14	US-10-227-884-78	Sequence 78, Appl
13	188	90.0	208	14	US-10-230-163-78	Sequence 78, Appl
14	188	90.0	208	14	US-10-230-338-78	Sequence 78, Appl
15	188	90.0	208	14	US-10-218-631-78	Sequence 78, Appl
16	188	90.0	208	14	US-10-230-414-78	Sequence 78, Appl
17	188	90.0	208	14	US-10-232-224-78	Sequence 78, Appl
18	188	90.0	208	14	US-10-216-159A-78	Sequence 78, Appl
19	188	90.0	208	14	US-10-218-849-78	Sequence 78, Appl
20	188	90.0	208	14	US-10-227-873-78	Sequence 78, Appl
21	188	90.0	208	14	US-10-227-883-78	Sequence 78, Appl
22	188	90.0	208	14	US-10-219-076-78	Sequence 78, Appl
23	188	90.0	208	14	US-10-230-434-78	Sequence 78, Appl
24	188	90.0	208	14	US-10-219-003-78	Sequence 78, Appl
25	188	90.0	208	14	US-10-219-075-78	Sequence 78, Appl
26	188	90.0	208	14	US-10-219-464-78	Sequence 78, Appl
27	188	90.0	208	14	US-10-219-466-78	Sequence 78, Appl
28	188	90.0	208	14	US-10-219-479-78	Sequence 78, Appl
29	188	90.0	208	14	US-10-219-481-78	Sequence 78, Appl
30	188	90.0	208	14	US-10-230-260-78	Sequence 78, Appl
31	188	90.0	208	14	US-10-232-231-78	Sequence 78, Appl
32	188	90.0	208	14	US-10-216-165-78	Sequence 78, Appl
33	188	90.0	208	14	US-10-218-956-78	Sequence 78, Appl
34	188	90.0	208	14	US-10-219-468-78	Sequence 78, Appl
35	188	90.0	208	14	US-10-219-478-78	Sequence 78, Appl
36	188	90.0	208	14	US-10-219-536-78	Sequence 78, Appl
37	188	90.0	208	14	US-10-233-205-78	Sequence 78, Appl
38	188	90.0	208	14	US-10-219-072-78	Sequence 78, Appl
39	188	90.0	208	14	US-10-219-470-78	Sequence 78, Appl
40	188	90.0	208	14	US-10-219-474-78	Sequence 78, Appl
41	188	90.0	208	14	US-10-219-524-78	Sequence 78, Appl
42	188	90.0	208	14	US-10-219-528-78	Sequence 78, Appl
43	188	90.0	208	14	US-10-227-880-78	Sequence 78, Appl
44	188	90.0	208	14	US-10-227-881-78	Sequence 78, Appl
45	188	90.0	208	14		

ALIGNMENTS

RESULT 1

US-09-822-485-24
; Sequence 24, Application US/09822485
; Patent No. US20020001825A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020001825A1uyuki
; TITLE OF INVENTION: NO. US20020001825A1el Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 08035.0001-01000
; CURRENT APPLICATION NUMBER: US/09/822.485
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Biochim. Biophys. Acta
; DATE: 2000
US-09-822-485-24

Query Match 100.0%; Score 209; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 4e-185;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDSDETFEHSGLVWVSLAGLLGACCAHPDSSPLLOFCGQVRQRYLYTDDAQOTEAH	60
Db	1	MDSDETFEHSGLVWVSLAGLLGACCAHPDSSPLLOFCGQVRQRYLYTDDAQOTEAH	60
Qy	61	LEIRDEGTGGAADQSPESLLOKALXPGVITQIGVKTSTRELCPQPCGALYGSLLHFDEA	120
Db	61	LEIRDEGTGGAADQSPESLLOKALXPGVITQIGVKTSTRELCPQPCGALYGSLLHFDEA	120
Qy	121	CSPRELLEDGYNVYQSEAHGLPLHLFGNKSPhRDPAAPRGPARFLPLGLPPALPEPPGI	180

Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209

RESULT 2

US-09-801-968-15
; Sequence 15, Application US/09801968
; Patent No. US20020082205A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020082205A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-17150.001/201130.40901
; CURRENT APPLICATION NUMBER: US/09/801,968
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-968-15

Query Match 100.0%; Score 209; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 4e-185;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209

RESULT 3

US-09-802-154-15
; Sequence 15, Application US/09802154
; Patent No. US20030105302A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20030105302A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-17149.001/201130.409
; CURRENT APPLICATION NUMBER: US/09/802,154
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-154-15

Query Match 100.0%; Score 209; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 4e-185;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209

RESULT 4

US-10-060-765-4
; Sequence 4, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060,765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-4

Query Match 100.0%; Score 209; DB 13; Length 209;
Best Local Similarity 100.0%; Pred. No. 4e-185;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLGLLGCQAHPIDSSPLLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIRDGTGGAADQSPESLLQKALKPGVITILGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGSPSQGRSPSYAS 209

RESULT 5

US-10-374-207-24
; Sequence 24, Application US/10374207
; Publication No. US20030170822A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20030170822A1uyuki
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses Thereof
; FILE REFERENCE: 08035.001-02000
; CURRENT APPLICATION NUMBER: US/10/374,207
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 09/822,485
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/540,118

; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; JOURNAL: Biochim. Biophys. Acta
 ; DATE: 2000
 ; US-10-374-207-24

Query Match	100.0%;	Score 209;	DB 14;	Length 209;
Best Local Similarity	100.0%;	Pred. No. 4e-185;		
Matches 209; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDSDGTGFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQVRORYLTTDAAQQTEAH	60	
Db	1	MDSDGTGFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQVRORYLTTDAAQQTEAH	60	
QY	61	LEIREDTGVGAADQSPESLLOLKALKPQVIQLGVKTSRFLCORPDGALYGSLLHFDEA	120	
Db	61	LEIREDTGVGAADQSPESLLOLKALKPQVIQLGVKTSRFLCORPDGALYGSLLHFDEA	120	
QY	121	CSFRELLRQGVNYQSEAHGLPLHLPGNKSPHRDPAPRGPARPLPGI,PPALPEPPGI	180	
Db	121	CSFRELLRQGVNYQSEAHGLPLHLPGNKSPHRDPAPRGPARPLPGI,PPALPEPPGI	180	
QY	181	LAPQPPDVGSSDPLSMVGPQGRSPSYAS	209	
Db	181	LAPQPPDVGSSDPLSMVGPQGRSPSYAS	209	

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RESULT 6
US-10-818-140-4
; Sequence 4, Application US/10818140
; Publication NO. US20040185494A1
; GENERAL INFORMATION:
; APPLICANT: Itch, Nobuyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGP-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/818.140
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-140-4

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	Query Match	100.0%;	Score 209;	DB 16;	Length 209;
	Best Local Similarity	100.0%;	Pred. No. 4e-185;		
	Matches 209;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDSDETGFEHSGIWSVLGALLGACQAHPIPDSSPLLQFGGQVRQRYLYTTDDAQQTEAH	60		
Db	1	MDSDETGFEHSGIWSVLGALLGACQAHPIPDSSPLLQFGGQVRQRYLYTTDDAQQTEAH	60		
QY	61	LEIREDTGVTGAADQSPESLLQLKALKPGYVQILGVKTSRFLCORPDGALYGSIHFDPEA	120		
Db	61	LEIREDTGVTGAADQSPESLLQLKALKPGYVQILGVKTSRFLCORPDGALYGSIHFDPEA	120		
QY	121	CSPRELLLEDGYNVYQSEAHGLPHLPGNKSPHRDPAPRGPARFLPLGPPALPPPPGI	180		
Db	121	CSPRELLLEDGYNVYQSEAHGLPHLPGNKSPHRDPAPRGPARFLPLGPPALPPPPGI	180		
QY	181	LAPQPPDVGSSDPLSMVGPQGRSPSYAS	209		

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Db      181 LAPQPDVGVSSDPLSMVGFSQGRSFSTAS 209

RESULT 7
US-10-771-173-4
; Sequence 4, Application US/10771173
; Publication No. US20050037457A1
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGR-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758 001/201130.408
; CURRENT APPLICATION NUMBER: US/10/771.173
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-173-4

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Query Match	100.0%	Score 209;	DB 17;	Length 209;
Best Local Similarity	100.0%;	Prod. No. 4e-185;		
Matches 209; Conservative	0;	Mismatches 0;	Indels 0	
Qy	1	MDSDETGFHSGLWVSVLAGLLIGACQAHPIPDSSFLQLQFGGQVQRXYLTDD		
Db	1	MDSDETGFHSGLWVSVLAGLLIGACQAHPIPDSSFLQLQFGGQVQRXYLTDD		
Qy	61	LEIREDTVGGAADQSPESLLQLKALKPGVQIQLGVKTSRFLCQRPDGALYGG		
Db	61	LEIREDTVGGAADQSPESLLQLKALKPGVQIQLGVKTSRFLCQRPDGALYGG		
Qy	121	CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPP		
Db	121	CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPP		
Qy	181	LAPQPPDVGSSDPLSMVGPSCGRSPSYAS	209	
Db	181	LAPQPPDVGSSDPLSMVGPSCGRSPSYAS	209	

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RESULT 8
US/10-659-004-68
/ Sequence 68, Application US/10659004
/ Publication No. US20050048507A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhong et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDE
/ FILE REFERENCE: 21402-608
/ CURRENT APPLICATION NUMBER: US/10/659,004
/ CURRENT FILING DATE: 2003-09-09
/ PRIORITY APPLICATION NUMBER: 60/295,607
/ PRIORITY FILING DATE: 2001-06-04
/ PRIORITY APPLICATION NUMBER: 60/295,661
/ PRIORITY FILING DATE: 2001-06-04
/ PRIORITY APPLICATION NUMBER: 60/296,404
/ PRIORITY FILING DATE: 2001-06-06
/ PRIORITY APPLICATION NUMBER: 60/296,418
/ PRIORITY FILING DATE: 2001-06-06
/ PRIORITY APPLICATION NUMBER: 60/297,414
/ PRIORITY FILING DATE: 2001-06-11
/ PRIORITY APPLICATION NUMBER: 60/297,567
/ PRIORITY FILING DATE: 2001-06-12
/ PRIORITY APPLICATION NUMBER: 60/298,285
/ PRIORITY FILING DATE: 2001-06-14
/ PRIORITY APPLICATION NUMBER: 60/298,556
/ PRIORITY FILING DATE: 2001-06-15
/ PRIORITY APPLICATION NUMBER: 60/299,949

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; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 68
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-68

Query Match      97.1%; Score 203; DB 17; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.4e-179;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  7 GFEHGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIRE 66
Db  7 GFEHGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIRE 66

Qy  67 GTVGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126
Db  67 GTVGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126

Qy  127 LLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPP 186
Db  127 LLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPP 186

Qy  187 DVGSSDPLSMVGPQGRSPSYAS 209
Db  187 DVGSSDPLSMVGPQGRSPSYAS 209

RESULT 9
US-10-659-004-70
; Sequence 70, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 70
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-70

Query Match      97.1%; Score 203; DB 17; Length 209;
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Best Local Similarity 100.0%; Pred. No. 1.4e-179;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  7 GFEHGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIRE 66
Db  7 GFEHGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIRE 66

Qy  67 GTVGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126
Db  67 GTVGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126

Qy  127 LLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPP 186
Db  127 LLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPP 186

Qy  187 DVGSSDPLSMVGPQGRSPSYAS 209
Db  187 DVGSSDPLSMVGPQGRSPSYAS 209

RESULT 10
US-10-659-004-66
; Sequence 66, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 66
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-66

Query Match      91.9%; Score 192; DB 17; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.2e-169;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  18 LAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIREDTVGGADOSP 77
Db  18 LAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOQTEAHLEIREDTVGGADOSP 77

Qy  78 ESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFRELLEDGYNVYQ 137
Db  78 ESLLQKALKPGVQILGVKTSRFLCQRPDGCALYSLHFDPEACSFRELLEDGYNVYQ 137

Qy  138 EAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPPVGSSDPLSNV 197
Db  138 EAHGLPLHLPGNKSPhRDPAPRGPARFLPLPGLPPALPEPPGILAPOPPVGSSDPLSNV 197
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Db 138 EAHGLPLHLPNGKSHRDPAPRGPARFLPLGLPALPEPPGILAPQPPDVSSDPLSMV 197
QY 198 GPSQGRSPSYAS 209
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Db 198 GPSQGRSPSYAS 209

RESULT 11
US-09-755-695-2
; Sequence 2, Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; FILE REFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09755,695
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/174,526
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2

Query Match 90.0%; Score 188; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.1e-165; Indels 0; Gaps 0;
Matches 188; Conservative 0; Mismatches 0;

QY 22 LLGACQAHPIPDSSFLQFGGQVRQRYLYTDDAQOQTEAHLEIREDTGTVGGADQSPESILL 81
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Db 21 LLGACQAHPIPDSSFLQFGGQVRQRYLYTDDAQOQTEAHLEIREDTGTVGGADQSPESILL 80
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QY 82 QLKALKPGVQILGLVKTSLRFLCQPDGALYGLSHFDPEACSPRELLLEDGYNVYQSEAHG 141
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Db 81 QLKALKPGVQILGLVKTSLRFLCQPDGALYGLSHFDPEACSPRELLLEDGYNVYQSEAHG 140
| | | | | | | | | |

QY 142 LPLHLPNGKSHRDPAPRGPARFLPLGLPALPEPPGILAPQPPDVSSDPLSMVGPQ 201
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Db 141 LPLHLPNGKSHRDPAPRGPARFLPLGLPALPEPPGILAPQPPDVSSDPLSMVGPQ 200
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QY 202 GRSPSYAS 209
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Db 201 GRSPSYAS 208
| | | | |

RESULT 12
US-10-227-884-78
; Sequence 78, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/100038
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; PRIOR APPLICATION NUMBER: 60/115558
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; PRIOR APPLICATION NUMBER: 60/130232
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; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445

; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
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; PRIOR APPLICATION NUMBER: 60/141037
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 90.0%; Score 188; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.le-165;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 LLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQTAAHLREIDGTGGADQSPESLL 81
Db 21 LLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQTAAHLREIDGTGGADQSPESLL 80

Qy 82 QLKALKEGVIQILGVKTSRFLCQPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAHG 141
Db 81 QLKALKEGVIQILGVKTSRFLCQPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAHG 140

Qy 142 LPLHLPGNKSHPRDPAFPGPARFLPLGLPALPEPPGILAPQPPDVCGSSDPLSNVGPQ 201
Db 141 LPLHLPGNKSHPRDPAFPGPARFLPLGLPALPEPPGILAPQPPDVCGSSDPLSNVGPQ 200

Qy 202 GRSPSYAS 209
Db 201 GRSPSYAS 208

RESULT 13
US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C96

;; CURRENT APPLICATION NUMBER: US/10/230,163
;; CURRENT FILING DATE: 2002-08-28
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
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;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
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;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
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;; PRIOR APPLICATION NUMBER: 60/081955
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;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
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;; PRIOR APPLICATION NUMBER: 60/130232
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 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 90.0%; Score 188; DB 14; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.1e-165;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 22 LLGCAQHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAHLEIRDTGTVGGADQSPESLL 81
 Db 21 LLGCAQHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAHLEIRDTGTVGGADQSPESLL 80
 Qy 82 QLKALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHG 141
 Db 81 QLKALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHG 140
 Qy 142 LPLHLPGNKSHPDRPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQ 201
 Db 141 LPLHLPGNKSHPDRPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQ 200
 Qy 202 GRSPSYAS 209
 Db 201 GRSPSYAS 208

RESULT 14
 US-10-338-78
 ; Sequence 78, Application US/10230338
 ; Publication No. US200300449341
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C92
 ; CURRENT APPLICATION NUMBER: US/10/230,338
 ; CURRENT FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
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 ; PRIOR APPLICATION NUMBER: 60/064103
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 ; PRIOR APPLICATION NUMBER: 60/069873
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 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 78
 ; LENGTH: 208
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-230-338-78

Query Match 90.0%; Score 188; DB 14; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.1e-165;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 22 LLGCAQHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAHLEIRDTGTVGGADQSPESLL 81
 Db 21 LLGCAQHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAHLEIRDTGTVGGADQSPESLL 80
 Qy 82 QLKALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHG 141
 Db 81 QLKALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHG 140
 Qy 142 LPLHLPGNKSHPDRPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQ 201
 Db 141 LPLHLPGNKSHPDRPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQ 200
 Qy 202 GRSPSYAS 209
 Db 201 GRSPSYAS 208

RESULT 15
 US-10-218-631-78
 ; Sequence 78, Application US/10218631
 ; Publication No. US20030045687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-78

Query Match          90.0%; Score 188; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.1e-165;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  22  LIGACQAHPIPDSSPLLQFGGQVRORYLYTDDAQQTAAHLEIREDTGCGAADQSPESLL 81
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Qy  21  LIGACQAHPIPDSSPLLQFGGQVRORYLYTDDAQQTAAHLEIREDTGCGAADQSPESLL 80
Db   |||||||
Qy  82  QLKALKPGVIOILGVKTSRFLCORPDGALYGSLEHDPACSFRELLLEDGYNVYQSEAHG 141
Db   |||||||
Qy  81  QLKALKPGVIOILGVKTSRFLCORPDGALYGSLEHDPACSFRELLLEDGYNVYQSEAHG 140
Db   |||||||
Qy  142  LPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPSQ 201
Db   |||||||
Qy  141  LPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPSQ 200
Db   |||||||
Qy  202  GRSPSYAS 209
Db   |||||||
Qy  201  GRSPSYAS 208
Db   |||||||
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Search completed: July 8, 2005, 23:04:40
Job time : 165 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:04:53 ; Search time 70.5375 Seconds
(without alignments)
221.182 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 1113
Sequence: 1 MDSDETFEHSGLWVSLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1113	100.0	209	4	US-09-715-805-4
2	1106	99.4	209	4	US-09-390-207-2
3	959	86.2	181	4	US-09-390-207-5
4	793.5	71.3	210	4	US-09-390-207-4
5	793.5	71.3	210	4	US-09-715-805-2
6	753	67.7	181	4	US-09-390-207-6
7	432	38.8	85	4	US-09-621-976-5213
8	265	23.8	216	4	US-09-907-794A-59
9	265	23.8	216	4	US-09-905-125A-59
10	265	23.8	216	4	US-09-902-775A-59
11	265	23.8	216	4	US-09-715-805-10
12	265	23.8	216	4	US-09-906-700-59
13	265	23.8	216	4	US-09-903-603A-59
14	265	23.8	216	4	US-09-904-920A-59
15	265	23.8	216	4	US-09-949-016-8206
16	265	23.8	216	4	US-09-909-064-59
17	265	23.8	216	4	US-09-905-381A-59
18	265	23.8	216	4	US-09-906-618-59
19	222.5	20.0	251	4	US-10-000-489-26
20	222.5	20.0	299	4	US-09-949-016-8018
21	206.5	18.6	216	4	US-09-715-805-9
22	201.5	18.1	134	4	US-09-621-976-4031
23	179	16.1	245	1	US-09-417-721-7
24	179	16.1	245	1	US-08-439-725A-11
25	179	16.1	245	2	US-08-867-471-11
26	179	16.1	245	2	US-08-438-439C-7
27	179	16.1	245	4	US-09-390-207-28

28	177.5	15.9	239	1	US-08-464-590A-11	Sequence 11, Appl
29	177.5	15.9	239	1	US-08-462-169B-11	Sequence 11, Appl
30	177.5	15.9	239	1	US-08-207-412B-14	Sequence 14, Appl
31	177.5	15.9	239	2	US-08-951-822-35	Sequence 35, Appl
32	177.5	15.9	239	3	US-09-103-079-11	Sequence 11, Appl
33	177.5	15.9	239	3	US-08-718-904-12	Sequence 12, Appl
34	177.5	15.9	239	3	US-09-023-082A-21	Sequence 21, Appl
35	177.5	15.9	239	3	US-09-093-585-11	Sequence 11, Appl
36	177.5	15.9	239	3	US-09-368-951-35	Sequence 35, Appl
37	177.5	15.9	239	4	US-09-425-021-11	Sequence 11, Appl
38	177.5	15.9	239	4	US-09-449-249-12	Sequence 12, Appl
39	177.5	15.9	239	4	US-09-390-207-18	Sequence 18, Appl
40	177.5	15.9	239	4	US-09-223-947-35	Sequence 35, Appl
41	177.5	15.9	239	4	US-09-564-829-5	Sequence 5, Appl
42	177.5	15.9	239	4	US-09-248-998-21	Sequence 21, Appl
43	177.5	15.9	239	4	US-09-572-406B-5	Sequence 5, Appl
44	177.5	15.9	239	4	US-09-610-651-21	Sequence 21, Appl
45	176.5	15.9	198	1	US-08-439-725A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-715-805-4
; Sequence 4, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715,805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-4

Query Match 100.0%; Score 1113; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.6e-100;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLQFGQVQRVLYTTDAQOTEAH	60
Db	1	MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLQFGQVQRVLYTTDAQOTEAH	60
Qy	61	LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDQALYGLHFDPEA	120
Db	61	LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDQALYGLHFDPEA	120
Qy	121	CSFRELLEDGVYVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPI	180
Db	121	CSFRELLEDGVYVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPI	180
Qy	181	LAPQPPDVGSSDPLSMVGPQGRSPSYAS	209
Db	181	LAPQPPDVGSSDPLSMVGPQGRSPSYAS	209

RESULT 2

US-09-390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371

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; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match      99.4%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.3e-99;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETGPHSGSLWTVLGLLGGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOQTEAH 60
   |||||
DB 1 MDSDETGPHSGSLWTVLGLLGGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOQTEAH 60

QY 61 LEIREDDGTGGAAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDQALYGSLSHFDPEA 120
   |||||
DB 61 LEIREDDGTGGAAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDQALYGSLSHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAREFLPLFGLPPALPEPGI 180
   |||||
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAREFLPLFGLPPALPEPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
   |||||
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 3
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match      86.2%; Score 959; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 2e-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 HPIDSSPLLQFGGQVRQRYLYTDDAQOQTEAHLEIREDDGTGGAAADQSPESLLQKALKP 88
   |||||
DB 1 HPIDSSPLLQFGGQVRQRYLYTDDAQOQTEAHLEIREDDGTGGAAADQSPESLLQKALKP 88

QY 89 GVIQILGVKTSRFLCQRPDQALYGSLSHFDPEACSFRELLEDGYNVYQSEAHGLPLHLPG 148
   |||||
DB 61 GVIQILGVKTSRFLCQRPDQALYGSLSHFDPEACSFRELLEDGYNVYQSEAHGLPLHLPG 120

QY 149 NKSPhRDPA PRGPAREFLPLFGLPPALPEPGIAPQPPDVGSSDPLSMVGPQGRSPSYA 208
   |||||
DB 121 NKSPhRDPA PRGPAREFLPLFGLPPALPEPGIAPQPPDVGSSDPLSMVGPQGRSPSYA 180

QY 209 S 209
DB 181 S 181

RESULT 4
US-09-390-207-4
; Sequence 4, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-4

Query Match      71.3%; Score 793.5; DB 4; Length 210;
Best Local Similarity 78.9%; Pred. No. 2.9e-69;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

QY 12 GLWYS-VIAGLLIGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOQTEAHLEIREDDGTVG 70
   |||||
DB 12 GLWVRLLLAVFLGLGYQAYPIPDSSPLLQFGGQVRQRYLYTDDQDQTEAHLEIREDDGTVG 71

QY 71 GAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDQALYGSLSHFDPEACSFRELLED 130
   |||||
DB 72 GAHRSPESSLELLELKALKPGVIQILGVKASRFLCQRPDQALYGSLSHFDPEACSFRELLED 131

QY 131 GYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAREFLPLFGLPPALPEPGIAPQPPDVGS 190
   |||||
DB 132 GYNVYQSEAHGLPLRLPQKDSFNQDATSWGVPVRLPMPGLLHLPDQAGFLPPEPPDVGS 191

QY 191 SDPLSMVGPQGRSPSYAS 209
   |||||
DB 192 SDPLSMVGPQGRSPSYAS 210

RESULT 5
US-09-715-805-2
; Sequence 2, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715,805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-715-805-2

Query Match      71.3%; Score 793.5; DB 4; Length 210;
Best Local Similarity 78.9%; Pred. No. 2.9e-69;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

QY 12 GLWYS-VIAGLLIGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOQTEAHLEIREDDGTVG 70
   |||||
DB 12 GLWVRLLLAVFLGLGYQAYPIPDSSPLLQFGGQVRQRYLYTDDQDQTEAHLEIREDDGTVG 71

QY 71 GAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDQALYGSLSHFDPEACSFRELLED 130
   |||||
DB 72 GAHRSPESSLELLELKALKPGVIQILGVKASRFLCQRPDQALYGSLSHFDPEACSFRELLED 131

QY 131 GYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAREFLPLFGLPPALPEPGIAPQPPDVGS 190
   |||||
DB 132 GYNVYQSEAHGLPLRLPQKDSFNQDATSWGVPVRLPMPGLLHLPDQAGFLPPEPPDVGS 191
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QY 191 SDPLSMVGPQGRSPSYAS 209
Db 192 SDPLSMVPLQGRSPSYAS 210

RESULT 6

US-09-390-207-6
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomson, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6

Query Match 67.7%; Score 753; DB 4; Length 181;
Best Local Similarity 80.7%; Pred. No. 2.1e-65;
Matches 146; Conservative 9; Mismatches 26; Indels 0; Gaps 0;
QY 29 HPIDSSPLQFGGVRQRYLYTDDAQTEAHLEIREDDGTGGAAQDQSPESLQKALKP 88
Db 1 YPIPDSSPLQFGGVRQRYLYTDDQDTEAHLEIREDDGTGGAAHRSPELLELQALKP 60
QY 89 GVIQILGVKTSRFLQCPDQALYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLP 148
Db 61 GVIQILGVKASRFLQCPDQALYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLP 120
QY 149 NKSHPDPAQRPAPRFLPLGLPPALPEPPGILAPPPDVGSDPLSMVGPQGRSPSYA 208
Db 121 KDSPNQDQATSMGVRFLPMPGLLHBPQDQAGLPPPEPPDVGSDPLSMVGPQGRSPSYA 180
QY 209 S 209
Db 181 S 181

RESULT 7

US-09-621-976-5213
; Sequence 5213, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala, Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu, Val

US-09-621-976-5213

Query Match 38.8%; Score 432; DB 4; Length 85;
Best Local Similarity 98.8%; Pred. No. 1.2e-34;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSLAGLLGACQAHPTDSSPLQFGGVRQRYLYTDDAQTEAH 60
Db 1 MDSDETFEHSGLWVSLAGLLGACQAHPTDSSPLQFGGVRQRYLYTDDAQTEAH 60
QY 61 LEIREDDGTGGAAQDQSPESLQK 84
Db 61 LEIREDDGTGGAAQDQSPESLQK 84

RESULT 8

US-09-907-794A-59
; Sequence 59, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564

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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-59

Query Match      23.8%; Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred. No. 6.9e-18;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;

QY 11  SGLWVSVLAGLLGCAQAHPIPDSSPLLQP--GQVQRQRYLYTDDAQ-QTEAHLEIRDGG 67
Db 14  AGLWLAV-AGRPLA-----FSDAGPHVHYGWDGPIRLRHLYTSGPHGLSSCFLIRADGG 66
QY 68  TVGGAADQSPESLIQLKALPGVLIQLGVKTSRFLCQRPDGCALYGSLSHFDPEACSPRELL 127
Db 67  VVDCARGQSAHSLLEIKAVALTVAIRGVSHSVRYLCMGADGWQGLQLQYSEEDCAFEFEI 126
QY 128 LEDGVNYVQSEAHGLPLHLPCNKSPHPRDPAKPGPARFLPLPGLPPALP-----EPPGI--- 180
Db 127 RPDGVNYVREKHLPLVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMVVEEPEDLRGH 182
QY 181 ----LAPQPPDVGDSSDPLSMV-GPSQGRSPSY 207
Db 183 LESDMFSSPLTSDMDPFGLVGTGEAVKRSPSF 214

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RESULT 9
US-09-905-125A-59
; Sequence 59, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Amkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A

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; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-59

Query Match 23.8%; Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred. No. 6.9e-18;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9

QY 11 SGHWVSVLGLLIGACQAHPIPDSSPLQF--GGVQRVLYTDDAQ-QTEAHLEIREDG 67
DB 14 AGMLTAV-AGRPLA-----FSDAGPHVHWGDPPIRLHLYTSGPHGLSCFPIRADG 66

QY 68 TVGGAADQPESLLQALKAPGVITQILGVKTSRFLCQRPDGGALYSGLSHFDPEACSFRELL 127
DB 67 VUDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLWCGADGKMOGLLQYSEEDCAFEESI 126

QY 128 LEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGARPLPLPGLPPALP-----EPPGI--- 180
DB 127 RPDGYNVYRSEKHRLPVLSLSAQ-QQLYKNRG---FLPLSHFLPLMPVWPEEPEDLRGH 182

QY 181 ----LAPQPDVCGSSDPLSMV-GPSQGRSPSY 207
DB 183 LESDMFSSPLETSDMDPFGLVLTGLEAVRSPSF 214

RESULT 10
US-09-902-775A-59
; Sequence 59, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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	Query Match	23.8%;	Score 265;	DB 4;	Length 216;	
	Best Local Similarity	36.3%;	Pred. No. 6.9e-18;			
	Matches	77;	Conservative	27;	Mismatches	82;
					Indels	26; Gaps
						9
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Db	14	AGLWLAV-AGRPLA-----PSDAGPHVYGWGDPIRLHLYTSGPHGUSSCFLRIRADG	66			
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Qy	68	TWVGAAQDSPELLOKALKEPQTQLGVKTSRFLCPDPGALYLGSHLPDPACSFRELL	127			
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Db	67	VVDCAQGSAHSLEIKVAALRTVAIKGVHSVRYLCGADKGKKQLLOYSEEDCAFEELI	126			
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Qy	128	LEDGYNVYOSEAHLPLHLPGNKNSPHRDPAAPRGPARFLPLFGLPALP----	EPGCI---	180		
		: :: :: :	:	:	:	:
Db	127	RPDGYNTVYSERHLPVSLSSAKO--RLYKNKG---FLPLSHFLPMLPMWPESPEDLRGH	182			
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-59

Query Match          23.8%   Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred. No. 6.9e-18;
Matches 77; Conservative 21; Mismatches 82; Indels 26; Gaps 9;

QY      11 SGLVSVSLAGLLGACQAHPIDPSSPLLQF--GGQVRQRVLYTTDDAQ-QTEAHLEIREDG 67
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DB      14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWGDPIRLHLHTSGPHGLSSCFLAIRADG 66

QY      68 TVCGAADQSPESSLQLKALPGVIQILGVTSRFLCORPDGALYGSLHFDPEACSFRELL 127
        :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB      67 VDCARGQSAHSLLLEIKNAVALRTVAIRKVSHSVRYLCMGADGMQGLLOYSEEDCAFEBSI 126

QY      128 LEDGYNVYQSEANGLPLHLPCNKSPHRDPAPRGPARFLPLGLPALP---EPGI--- 180
        :|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB      127 RPDGYNVYRKRLPVLSLAKQ-ROLYKNRG---FLPLSHFLPMLPMVPPEEDLRGH 182

QY      181 ----LAQPQPDVGSSDPLSNV-GPSQGRSPSY 207
        :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB      183 LESDMFSSPLETDSMDPFGLVTGLEAVRSPSP 214

RESULT 15
US-09-949-016-8206
; Sequence 8206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 8206
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8206

Query Match 23.8%; Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred.No. 6.9e-18;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;
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Db 14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWDPIRLRLHLYTSGPHGLSSCFLIRADG 66
Qy 68 TVGGAADQSPESLLQLKALKPGVIOILGVKTSRFLCORPDGALYGSLLHFDPEACSFRELL 127
Db 67 VVDCARGQSAHSLLEIKAVALTVAIKGVHSVRLCMGADGKMQGLLYSEEDCAFEFEI 126
Qy 128 LEDGYNVYQSEAHGILPLHLPGNKSPHRDPAPRGPARFLPLPCLPALP---EPPGI--- 180
Db 127 RPDGYNVYRSEKHRLFVLSLAKQ-RQLYKNRG---FLPLSHFLPMLPMVPEPEDLURGH 182
Qy 181 ----LAPQPPDVGSSDPLSMV-GPSQGRSPSY 207
Db 183 LESDMFSSPLETDSMDPFLVTGLEAVRSPSF 214

Search completed: July 8, 2005, 22:22:32
Job time : 72.5375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:18:21 ; Search time 249.058 Seconds
(without alignments)
324.193 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 1113

Sequence: 1 MDSDETFEHSGLMVSLAG.....SSDPLSMVSPGQGRSPSYAS 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1113	100.0	209	9	US-09-822-485-24
2	1113	100.0	209	9	US-09-801-968-15
3	1113	100.0	209	10	US-09-802-154-15
4	1113	100.0	209	13	US-10-060-765-4
5	1113	100.0	209	14	US-10-374-207-24
6	1113	100.0	209	16	US-10-818-140-4
7	1113	100.0	209	17	US-10-771-173-4
8	1109	99.6	209	17	US-10-659-004-62
9	1109	99.6	209	17	US-10-659-004-66
10	1108	99.6	209	17	US-10-659-004-70
11	1107	99.5	209	17	US-10-659-004-68

12	1107	99.5	209	17	US-10-659-004-72	Sequence 72, Appl
13	1107	99.5	209	17	US-10-659-004-74	Sequence 74, Appl
14	1106	99.4	209	9	US-09-799-776-2	Sequence 2, Appl
15	1106	99.4	209	17	US-10-659-004-56	Sequence 56, Appl
16	1106	99.4	209	17	US-10-659-004-58	Sequence 58, Appl
17	1106	99.4	209	17	US-10-659-004-64	Sequence 64, Appl
18	1098.5	98.7	208	9	US-09-755-695-2	Sequence 2, Appl
19	1098.5	98.7	208	14	US-10-227-884-78	Sequence 78, Appl
20	1098.5	98.7	208	14	US-10-230-163-78	Sequence 78, Appl
21	1098.5	98.7	208	14	US-10-230-338-78	Sequence 78, Appl
22	1098.5	98.7	208	14	US-10-218-631-78	Sequence 78, Appl
23	1098.5	98.7	208	14	US-10-230-414-78	Sequence 78, Appl
24	1098.5	98.7	208	14	US-10-232-224-78	Sequence 78, Appl
25	1098.5	98.7	208	14	US-10-216-159A-78	Sequence 78, Appl
26	1098.5	98.7	208	14	US-10-218-849-78	Sequence 78, Appl
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29	1098.5	98.7	208	14	US-10-219-076-78	Sequence 78, Appl
30	1098.5	98.7	208	14	US-10-230-434-78	Sequence 78, Appl
31	1098.5	98.7	208	14	US-10-219-003-78	Sequence 78, Appl
32	1098.5	98.7	208	14	US-10-219-075-78	Sequence 78, Appl
33	1098.5	98.7	208	14	US-10-219-464-78	Sequence 78, Appl
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37	1098.5	98.7	208	14	US-10-230-260-78	Sequence 78, Appl
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41	1098.5	98.7	208	14	US-10-218-956-78	Sequence 78, Appl
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43	1098.5	98.7	208	14	US-10-219-478-78	Sequence 78, Appl
44	1098.5	98.7	208	14	US-10-219-536-78	Sequence 78, Appl
45	1098.5	98.7	208	14	US-10-233-205-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1

US-09-822-485-24
; Sequence 24, Application US/09822485
; Patent No. US20020001825A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020001825A1
; TITLE OF INVENTION: NO. US20020001825A1el Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 08035.0001-01000
; CURRENT APPLICATION NUMBER: US/09/822.485
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Biochim. Biophys. Acta
; DATE: 2000
US-09-822-485-24

Query Match		100.0%	Score 1113;	DB 9;	Length 209;
Best Local Similarity		100.0%	Pred. No. 1.5e-83;		
Matches 209;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MDSDETFEHSGLMVSLAGLLLCACAHPTPDS	SPLLQFCGOVQRVLYTDDAQOTEAH	60	
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Qy	61	LEIREDTGVGAADQSPESLIQLKALPGVITQI	LGKTSRFLCQRPDGCALYGSLSHFDEA	120	
Db	61	LEIREDTGVGAADQSPESLIQLKALPGVITQI	LGKTSRFLCQRPDGCALYGSLSHFDEA	120	
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RESULT 2
US-09-801-968-15
; Sequence 15, Application US/09801968
; Patent No. US20020082205A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020082205A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-17150.001/201130.40901
; CURRENT APPLICATION NUMBER: US/09/801,968
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-968-15

Query Match 100.0%; Score 1113; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LEIREDTGVGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
Qy 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 3
US-09-802-154-15
; Sequence 15, Application US/09802154
; Publication No. US20030105302A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20030105302A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-17149.001/201130.409
; CURRENT APPLICATION NUMBER: US/09/802,154
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-154-15

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Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVRQRYLYTDDAQOTEAH 60
Qy 61 LEIREDTGVGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
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Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
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RESULT 4
US-10-060-765-4
; Sequence 4, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060,765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-4

Query Match 100.0%; Score 1113; DB 13; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVRQRYLYTDDAQOTEAH 60
Qy 61 LEIREDTGVGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPARFLPLGLPPALPEPPI 180
Qy 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 5
US-10-374-207-24
; Sequence 24, Application US/10374207
; Publication No. US20030170822A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20030170822A1uyuki
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses Thereof
; FILE REFERENCE: 08035.0001-02000
; CURRENT APPLICATION NUMBER: US/10/374,207
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 09/822,485
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/540,118
```

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; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Biochim. Biophys. Acta
; DATE: 2000
; US-10-374-207-24

Query Match      100.0%; Score 1113; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDSDETCFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQRORYLYTTDDAQOTEAH 60
DB      1 MDSDETCFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQRORYLYTTDDAQOTEAH 60
QY      61 LEIREDTGVCGAADOQSPESLLQLKALKEGVTIQLGVKTSRFLCQRPDQALYGSLLHFDPEA 120
DB      61 LEIREDTGVCGAADOQSPESLLQLKALKEGVTIQLGVKTSRFLCQRPDQALYGSLLHFDPEA 120
QY      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPA PRGPAREFLPLPGLPPALPEPFGI 180
DB      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPA PRGPAREFLPLPGLPPALPEPFGI 180
QY      181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB      181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 6
US-10-818-140-4
; Sequence 4, Application US/10818140
; Publication No. US20040185494A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, Nobuyuki
; APPLICANT: Kavanagh, W. Michael
; TITLE OF INVENTION: HUMAN EGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/818,140
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-818-140-4

Query Match      100.0%; Score 1113; DB 16; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDSDETCFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQRORYLYTTDDAQOTEAH 60
DB      1 MDSDETCFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGVQRORYLYTTDDAQOTEAH 60
QY      61 LEIREDTGVCGAADOQSPESLLQLKALKEGVTIQLGVKTSRFLCQRPDQALYGSLLHFDPEA 120
DB      61 LEIREDTGVCGAADOQSPESLLQLKALKEGVTIQLGVKTSRFLCQRPDQALYGSLLHFDPEA 120
QY      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPA PRGPAREFLPLPGLPPALPEPFGI 180
DB      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPA PRGPAREFLPLPGLPPALPEPFGI 180
QY      181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

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; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 62
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-62

Query Match
Best Local Similarity 99.6%; Score 1109; DB 17; Length 209;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 9
US-10-659-004-66
; Sequence 66, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 66
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-66

Query Match
Best Local Similarity 99.6%; Score 1109; DB 17; Length 209;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
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```
Best Local Similarity 99.5%; Pred. No. 3.1e-83;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 10
US-10-659-004-70
; Sequence 70, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 70
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-70

Query Match
Best Local Similarity 99.6%; Score 1108; DB 17; Length 209;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQLQFGGVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
Db 61 LEIREDTGVGAADQSPESLLQLKALKPGVQIILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
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Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI 180
Qy 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209

RESULT 11

US-10-659-004-68
; Sequence 68, Application US/10659004
; Publication No. US20050048507A1

; GENERAL INFORMATION:

; APPLICANT: Zhong et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-608

; CURRENT APPLICATION NUMBER: US/10/659,004

; PRIOR FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/297,414

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 60/297,567

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/298,285

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298,556

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/299,949

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/300,883

; PRIOR FILING DATE: 2001-06-26

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 187

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 68

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-659-004-68

Query Match 99.5%; Score 1107; DB 17; Length 209;

Best Local Similarity 99.5%; Pred. No. 4.5e-83;

Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQTEAH 60
Db 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQTEAH 60

Qy 61 LEIREDTGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYSLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYSLHFDPEA 120

Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI 180

Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI 180

Qy 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209

Db 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209

RESULT 12

US-10-659-004-72

; Sequence 72, Application US/10659004

; Publication No. US20050048507A1

; GENERAL INFORMATION:

; APPLICANT: Zhong et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-608

; CURRENT APPLICATION NUMBER: US/10/659,004

; PRIOR FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/297,414

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 60/297,567

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/298,285

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298,556

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/299,949

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/300,883

; PRIOR FILING DATE: 2001-06-26

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 187

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 72

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-659-004-72

Query Match 99.5%; Score 1107; DB 17; Length 209;

Best Local Similarity 99.5%; Pred. No. 4.5e-83;

Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQTEAH 60

Db 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQTEAH 60

Qy 61 LEIREDTGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYSLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYSLHFDPEA 120

Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI 180

Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI 180

Qy 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209

Db 181 LAPQPPDVGSSDPLSMVGFSGQSRSPSYAS 209

RESULT 13

US-10-659-004-74

; Sequence 74, Application US/10659004

; Publication No. US20050048507A1

; GENERAL INFORMATION:

; APPLICANT: Zhong et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-608

; CURRENT APPLICATION NUMBER: US/10/659,004

; PRIOR FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/297,414

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; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 74
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-74

Query Match      99.5%; Score 1107; DB 17; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.5e-83;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60
Db      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60

QY      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120
Db      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120

QY      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180
Db      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180

QY      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
```

```
RESULT 14
US-09-799-776-2
; Sequence 2, Application US/09799776
; Patent No. US20010012628A1
; GENERAL INFORMATION:
; APPLICANT: Pankaj Agarwal
; APPLICANT: Frank Barone
; APPLICANT: John A. Feild
; APPLICANT: Karen S. Kabnick
; APPLICANT: Michael S. McQueney
; TITLE OF INVENTION: sbgFGF-19a
; FILE REFERENCE: GP-70659-C1
; CURRENT APPLICATION NUMBER: US/09/799,776
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 09/434,358
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-799-776-2

Query Match      99.4%; Score 1106; DB 9; Length 209;
Best Local Similarity 99.5%; Pred. No. 5.5e-83;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60
Db      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60
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QY      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120
Db      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120

QY      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180
Db      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180

QY      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
```

```
RESULT 15
US-10-659-004-56
; Sequence 56, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 56
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-56

Query Match      99.4%; Score 1106; DB 17; Length 209;
Best Local Similarity 99.5%; Pred. No. 5.5e-83;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60
Db      1 MDSDETGFEHSGLMWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTTDDAQQTEAH 60

QY      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120
Db      61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120

QY      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180
Db      121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLGLPPALPEPPGI 180

QY      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db      181 LAQPPDVGSSDPLSMVGPQGRSPSYAS 209
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Search completed: July 8, 2005, 22:44:49
Job time : 250.058 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:03:50 ; Search time 51.3792 Seconds
(without alignments)
391.390 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 1113
Sequence: 1 MDSUTGFHSGLWVSLAG.....SSDPLSMVGPQGRSPSYAS 209
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249.5	22.4	251	2 JC7513	fibroblast growth
2	179	16.1	245	1 TVMST2	transforming prote
3	177.5	15.9	239	1 S04742	fibroblast growth
4	176.5	15.9	208	2 S20102	fibroblast growth
5	174	15.6	187	2 S23595	embryonic fibrobla
6	173	15.5	206	2 JC4268	fibroblast growth
7	170.5	15.3	208	2 S14192	fibroblast growth
8	167	15.0	266	2 S68144	fibroblast growth
9	165	14.8	194	2 IS0710	fibroblast growth
10	164	14.7	264	2 A36207	fibroblast growth
11	163.5	14.7	192	2 S54407	embryonic fibrobla
12	163.5	14.7	206	1 TVHUS	fibroblast growth
13	161	14.5	211	2 JC7353	fibroblast growth
14	160.5	14.4	256	2 JC4627	fibroblast growth
15	160	14.4	212	2 JC7511	fibroblast growth
16	157	14.1	208	2 S6486	fibroblast growth
17	157	14.1	208	2 A48137	fibroblast growth
18	155.5	14.0	155	1 A60721	acidic fibroblast
19	148.5	13.9	155	2 D37360	acidic fibroblast
20	154.5	13.9	155	2 S04147	acidic fibroblast
21	153.5	13.8	202	1 TVMHS	fibroblast growth
22	153	13.7	208	2 JC7082	fibroblast somatot
23	150.5	13.5	207	2 JC5941	fibroblast growth
24	148.5	13.3	267	1 TVHUF5	fibroblast growth
25	146.5	13.2	155	1 A33665	acidic fibroblast
26	146.5	13.2	207	2 JC5940	fibroblast growth
27	146	13.1	237	1 S39582	transforming prote
28	144.5	13.0	155	1 GRBOA	acidic fibroblast
29	143.5	12.9	152	2 JH0476	acidic fibroblast

30	142	12.8	194	2 S26049	fibroblast growth
31	142	12.8	220	2 S26049	fibroblast growth
32	141	12.7	194	2 S49501	keratinocyte growt
33	140	12.6	194	2 I48610	keratinocyte growt
34	139	12.5	194	1 A36301	fibroblast growth
35	138	12.4	189	2 A48834	basic fibroblast g
36	135	12.1	155	1 A40117	basic fibroblast g
37	131.5	11.8	155	2 JWO055	acidic fibroblast
38	127.5	11.5	155	2 A60130	acidic fibroblast
39	127	11.4	164	2 S31622	basic fibroblast g
40	124	11.1	413	2 H88481	protein let-756 (i
41	122	11.0	154	2 C37360	basic fibroblast g
42	122	11.0	154	2 A31674	basic fibroblast g
43	122	11.0	168	2 JG0184	fibroblast growth
44	121	10.9	137	2 I46711	fibroblast growth
45	121	10.9	146	1 S00185	basic fibroblast g

ALIGNMENTS

RESULT 1

JC7513
fibroblast growth factor-23 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7513
R:Yamashita, T.; Yoshioaka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A:Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially exp.
A:Reference number: JC7513; MUID:20490027; PMID:11032749
A:Contents: Embryo
A:Accession: JC7513
A:Molecule type: mRNA
A:Residues: 1-251 <YAM>
A:Cross-references: UNIPROT:Q9BPC2; DBJ:AB037889
C:Comment: This factor, a secreted protein, acts on proximal cells and plays roles in tr
C:Genetics:
A:Gene: fgf-23
C:Keywords: nucleus

Query Match	22.4%;	Score	249.5;	DB 2;	Length	251;	
Best Local Similarity	35.1%;	Pred. No.	1.1e-12;				
Matches	73;	Conservative	27;	Mismatches	85;	Gaps	8;
QY	12	GLWVSVLGLLIGACQ---AHPIDSSPLL--QFGQVQRQRYLYTDDAQQTAEHLEIRE	66				
Db	3	GTCLLLVGLVCTVCSLGTARAYPTSPLLGSNWGSLT---HLYTATA-RTSYHLQIHRD	58				
QY	67	GTVGAADQSPESLLQLKALKPGVITQILGVKTSRPLCORPDGALYGSLLHFDPA	126				
Db	59	GHVDGTPHOTIYSALMITSEDAGSVITGAMTRRFLCMDLHGNIFGSLHFS	118				
QY	127	LLEDGVNYQSEAHGLPLHLPGNK---SPHRDPAPRGAPRL-----PLPGLPALPEP	177				
Db	119	TLENGIDVYLSQKHVLYSLGRAKRIFQGNPPPF--SQFLARNEVPLLHFTVTRPR	176				
QY	178	PGILAPQPPDVGSSDPLSMVGPQGRSP	205				
Db	177	HTRSADDPPE---RDPLNVLKPRRATP	201				

RESULT 2

TVMST2
transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
EMBO J. 5, 919-924, 1986
A:Title: Sequence, topography and protein coding potential of mouse int-2: a putative or
A:Reference number: A23930; MUID:86247582; PMID:3013624
A:Accession: A23930

A;Molecule type: DNA; mRNA
A;Residues: 1-245 <MO>
A;Cross-references: UNIPROT:P05524; GB:Y00848; GB:M26284; GB:X68450; NID:G52716; PIDN:CA
R;Acland, P.; Dixon, M.; Peters, G.; Dickson, C.
A;Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation
A;Reference number: S08157; MUID:90158795; PMID:2406607
A;Accession: S08157
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'HSRAGLARGVLPAPRLRETRAGAAAAGGRDAGM', 3-17 <ACI>
C;Genetics:
A;Gene: int-2
A;Map position: 7
A;Introns: 74/1; 108/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein

Query Match 16.1%; Score 179; DB 1; Length 245;
Best Local Similarity 28.8%; Pred. No. 4.3e-07;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSR 100
DB 40 GGAPRRKLYC-----ATKYHLQLHPSGRVNGSLNSAYSILEITAVEGVVAIKGLPSGR 95

QY 101 FLCQPDGALYGLSHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPKNKSP--HRDPAP 158
DB 96 YLAMNKRGLYASDHYNAE-CEFVERIHELGYNTYASR-----LYRTSGSGFGAQRQPGA 149

QY 159 RGP-----ARFLPLGLPPALPEPPGILAQPPDVGSSDPLSMVPGSQSPSPVAS 209
DB 150 QRPVTVSVNGKRRPRGRGFKTRTKQSSSLFLPRVLGHKDHWMRLQLQSSQPRAPCEGS 206

RESULT 3
S04742
fibroblast growth factor 3 precursor - human
N;Alternate names: transforming protein int-2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S04742
R;Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.
Oncogene 4, 429-436, 1989
A;Title: Sequence organization of the human int-2 gene and its expression in teratocarci
A;Reference number: S04742; MUID:89239468; PMID:2470007
A;Accession: S04742
A;Molecule type: DNA
A;Residues: 1-239 <BRO>
A;Cross-references: UNIPROT:P11487; EMBL:X14445; NID:G33937; PIDN:CAA32615.1; PID:G31240
C;Genetics:
A;Gene: GDB:FGF3; INT2
A;Cross-references: GDB:120103; OMIM:164950
A;Map position: 11q13.3-11q13.3
A;Introns: 74/1; 108/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-239/Product: transforming protein (int-2) #status predicted <MAT>

Query Match 15.9%; Score 177.5; DB 1; Length 239;
Best Local Similarity 29.7%; Pred. No. 5.5e-07;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSR 100
DB 40 GGAPRRKLYC-----ATKYHLQLHPSGRVNGSLNSAYSILEITAVEGVVAIKGLPSGR 95

QY 101 FLCQPDGALYGLSHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPKNKSPHRDPAP-- 158
DB 96 YLAMNKRGLYASDHYNAE-CEFVERIHELGYNTYASRLYRTVSTTPGAR---RQPSAER 151

QY 159 -----RGPAR-----FLP-----LPGLPPALPEPPG 179

DB 152 LMYTVSVNGKRRPRGRGFKTRTKQSSSLFLPRVLGHRDHWMYRQLQSLGPRPG 203

RESULT 4
S20102
fibroblast growth factor 6 precursor - human
N;Alternate names: fibroblast growth factor-related protein FGF.6; transforming protein
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S20102; S23739; S04204; S36910
R;Coulrier, F.; Batoz, M.; Marics, I.; de Lapeyriere, O.; Birnbaum, D.
Oncogene 6, 1437-1444, 1991
A;Title: Putative structure of the FGF6 gene product and role of the signal peptide.
A;Reference number: S20102; MUID:91360279; PMID:1886714
A;Accession: S20102
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-208 <COU>
A;Cross-references: UNIPROT:P10767; EMBL:X57075
A;Note: it is uncertain whether Met-1, Met-11 or Met-34 is the initiator
R;Iida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Sato, T.; On
Oncogene 7, 303-309, 1992
A;Title: Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.
A;Reference number: S23739; MUID:92195660; PMID:1549352
A;Accession: S23739
A;Molecule type: mRNA
A;Residues: 1-208 <IID>
A;Cross-references: EMBL:X63454
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;Marics, I.; Adelaide, J.; Raybaud, F.; Mattei, M.G.; Coulrier, F.; Planche, J.; de Lape
Oncogene 4, 335-340, 1989
A;Title: Characterization of the HST-related FGF.6 gene, a new member of the fibroblast
A;Reference number: S04204; MUID:89201880; PMID:2649847
A;Accession: S04204
A;Molecule type: DNA
A;Residues: 81-99 'G', 101-208 <MAR>
A;Cross-references: EMBL:X14071; NID:G31354; PIDN:CAB37648.2; PID:G4467836
C;Genetics:
A;Gene: GDB:FGF6; hst-2
A;Cross-references: GDB:119908; OMIM:134921
A;Map position: 12p13-12p13
A;Introns: 115/3; 150/2
C;Superfamily: fibroblast growth factor
F;1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted <SIG>
F;41-208/Product: fibroblast growth factor 6 #status predicted <MAT>

Query Match 15.9%; Score 176.5; DB 2; Length 208;
Best Local Similarity 29.1%; Pred. No. 5.7e-07;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLIGACQAHF-----IPDS---SPLIQ-----FGQV----- 44
DB 22 LNALVFLGILGVVVPSPAGTRANNITLDSRGWGTLLSRAGLAGETAGYNWESGYLVG 81

QY 45 --RQRYLYTDDAQOQTEAHLEIREDTGTVGGAADQSPESLLQKALKPGVIQILGVKTSRFL 102
DB 82 IKRQRYLYCNVG--IGFHLQVLPDGRISGTHTHEPNYSLLLEISTVERGVWSLFGVRSALFV 139

QY 103 CORPDGALYGLSHFDPEACSFRELLLEDGYNVYQSEAH 140
DB 140 AMNSKGRLYATPSPFQ-ECKEFRETLPPNNYNAYESDLY 176

RESULT 5
S23595
embryonic fibroblast growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23595
R;Issacs, H.V.; Tannahill, D.; Slack, J.M.W.
Development 114, 711-720, 1992
A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing facto

A:Reference number: S23595; MUID:92315916; PMID:1618138

A:Accession: S23595

A:Molecule type: mRNA

A:Residues: 1-187 <ISA>

A:Cross-references: UNIPROT:P48805; EMBL:X62593; PIDN:CAA44479.1; PID:g64693

C:Superfamily: fibroblast growth factor

Query Match 15.6%; Score 174; DB 2; Length 187;
Best Local Similarity 34.8%; Pred. No. 7.9e-07;
Matches 48; Conservative 23; Mismatches 57; Indels 10; Gaps 5;

QY 33 DSSPLLQGGQVRQRYLYTDDAQOTEAHLEIREDTGVCAGDQSPESLLQKALKPGVVIQ 92
DB 54 DSDYLL---GIKQRRLYCNVG--IGFHIQVLPDGRINGMSSENYSLLESPVGVVS 108
QY 93 ILGVTSRFLCQRPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAH-GLPLHLPGN-- 149
DB 109 LVGVKSGMFVAMNAKGLYGRYFN-ECKPKETLLPNNYAYESKYPGMVIALGKNGR 167
QY 150 -KSPHRDPAPRGPARFLP 166
DB 168 TKGNRVSPPTMTLTFLP 185

RESULT 6

JC4268
fibroblast growth factor 4 - bovine
N:Alternate names: transforming protein hst
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
A:Accession: JC4268
R:Yu, J.C.; Desseabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heidaran, Gene 162, 333-334, 1995
A:Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A:Reference number: JC4268; MUID:96032369; PMID:7557455

A:Accession: JC4268

A:Molecule type: mRNA

A:Residues: 1-206 <YUJ>

A:Cross-references: GB:U15969

A:Note: The authors translated the codon GGC for residue 114 as Ser

C:Comment: This protein is a member of fibroblast growth factor family. The hst gene in c

C:Genetics:

A:Gene: hst

A:Introns: 113/3; 145/2

C:Superfamily: fibroblast growth factor

C:Keywords: thymus; transforming protein

Query Match 15.5%; Score 173; DB 2; Length 206;
Best Local Similarity 31.5%; Pred. No. 1.1e-06;
Matches 51; Conservative 23; Mismatches 76; Indels 12; Gaps 5;

QY 14 WSVVLGELLGACQAHPIPDSPLLQGGQV-----RQRYLYTDDAQOTEAHLEIREDTG 68
DB 46 WESLVARSLLAGLPVAPQKERAUVSGAGDYLLGKRLRLYCNVG--IGFHLQVLPDGR 103

QY 69 VGGADQSPESLLQKALKPGVVIQILGKTRFLCQRPDQALYGLSHFDPEACSFRELL 128
DB 104 IGGVHADTSDGLELSPVERGVISFVASRFFVAMSSRGLYSPFTDGE-CRPREILL 162

QY 129 EDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166

DB 163 PNNYAYECDRHPGFMIALSKNGKAKGNRVSPPTMKVTHFLP 204

RESULT 7

S14192
fibroblast growth factor 6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: S14192; I49665; I49664
R:de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche, J. Oncogene 5, 823-831, 1990
A:Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.

A:Reference number: S14192; MUID:90295275; PMID:2193291

A:Accession: S14192

A:Molecule type: DNA

A:Residues: 1-208 <LAP>

A:Cross-references: UNIPROT:P21658; EMBL:X51552

A:Note: it is uncertain whether Met-1 or Met-11 is the initiator

R:Ollendorff, V.; Rosnet, O.; Marice, I.; Birnbaum, D.; deLapeyriere, O.

Biochimie 74, 1035-1038, 1992

A:Title: Isolation and sequence of the murine Fgf6 cDNA.

A:Reference number: I49664; MUID:93120244; PMID:1477139

A:Accession: I49665

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 19-208 <RES>

A:Cross-references: GB:M92416; NID:G193288; PIDN:AAA62261.1; PID:g666915

A:Accession: I49664

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RE2>

A:Cross-references: GB:M92415; NID:G193286; PIDN:AAA62260.1; PID:g193287

C:Genetics:

A:Gene: Fgf6

A:Introns: 116/1; 150/3

C:Superfamily: fibroblast growth factor

Query Match 15.3%; Score 170.5; DB 2; Length 208;
Best Local Similarity 36.4%; Pred. No. 1.7e-06;
Matches 36; Conservative 21; Mismatches 39; Indels 3; Gaps 2;

QY 42 GQVQRVLYTDDAQOTEAHLEIREDTGVCAGDQSPESLLQKALKPGVVIQILGKTRSP 101

DB 81 GIKQRRLYCNVG--IGFHIQVLPDGRISGTHSENPYSLLEISTVERGVSLFGVKSALP 138

QY 102 LCQRPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAH 140

DB 139 IAMSKGRLYTPSFHDE-CKFRETLLENYAYESDLY 176

RESULT 8

S68144

fibroblast growth factor 5 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

A:Accession: S68144

R:Hattori, Y.; Yamasaki, M.; Itoh, N.

Biochim. Biophys. Acta 1306, 31-33, 1996

A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel tr

A:Reference number: S68144; MUID:96201703; PMID:8611621

A:Accession: S68144

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-266 <HAT>

A:Cross-references: UNIPROT:P48807; EMBL:D64085; NID:G992952; PIDN:BAA10966.1; PID:g99292

C:Superfamily: fibroblast growth factor

Query Match 15.0%; Score 167; DB 2; Length 266;
Best Local Similarity 30.3%; Pred. No. 4.3e-06;
Matches 63; Conservative 26; Mismatches 69; Indels 50; Gaps 11;

QY 34 SSPLLQGGQVRQRYLYTDDAQOTE-----HLEIREDTGVCAGDQSPESLLQK 84

DB 63 ASPGSGSGSRHSSFGWSPSGRRTGSLYCRVIGIQLQIYDPDKVNGSHEASVLSILRIF 122

QY 85 ALKPGVVIQILGKTRFLCQRPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAH---- 140

DB 123 AVSQGIVGIRVFNKFLAMSKKGLHASAKFTDD-CKFRERFQENSYNTYASAIHRTK 181

QY 141 -GLPLHLPGNKSHPDRPAPRG-----PARFLP-----LFGLP-----PALP 178

DB 182 TGREYVALNK--RGAKRCCSPRVKQHVSTHFLPRFKQSEQPELSFTVTVPKCKPP 238

QY 179 GILAPQPDVGSDDLPMVSGVSGQRSPS 206

A:Reference number: A29876; MUID:87204251; PMID:2953031

A:Accession: A29876

A:Molecule type: mRNA

A:Residues: 1-206 <TAI>

A:Cross-references: GB:J02986; GB:M16338; NID:g184430; PIDN:AA859555.1; PID:g386788

R:Deilli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.

Cell 50, 729-737, 1987

A:Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth factor

A:Reference number: A29649; MUID:87301716; PMID:2957062

A:Accession: A29649

A:Molecule type: mRNA

A:Residues: 1-206 <BOV>

A:Cross-references: GB:M17446; NID:g186785; PIDN:AA59473.1; PID:g307092

C:Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mouse

C:Genetics:

A:Gene: GDB:FGF4; HSTF1

A:Cross-references: GDB:120066; OMIM:164980

A:Map position: 11q13.3-11q13.3

A:Introns: 114/1; 148/3

C:Superfamily: fibroblast growth factor

C:Keywords: growth factor; Kaposi sarcoma; transforming protein

Query Match 14.7%; Score 163.5; DB 1; Length 206;

Best Local Similarity 36.9%; Pred. No. 6e-06; Mismatches 46; Indels 5; Gaps 3;

Matches 41; Conservative 19; Mismatches 46; Indels 5; Gaps 3;

Qy 60 HLEIREDTGVGAADQSPESLQKALPGVQIILGVKTSRFLCQRPDGLYGLSLHFDPE 119

Db 95 HLOALPDGRIIGAHADTRDSLELSPVERGVVIFGVASRFVMSKGLYGSPPFTDE 154

Qy 120 ACSFRELLEDGYNVQSEAH-GLPLHLPGN---KSPHRDPAPRGAPPLP 166

Db 155 -CTFKELLPNYNAYESKYPGMPIALSKNGKTKGNRVSPMTKVTFLP 204

RESULT 13

JC7353

fibroblast growth factor-20 - human

C:Species: Homo sapiens (man)

C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004

C:Accession: JC7353

R:Kirikoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiokawa, K.; Katoh,

Biochem. Biophys. Res. Commun. 274, 337-343, 2000

A:Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-p22

A:Reference number: JC7353

A:Accession: JC7353

A:Molecule type: mRNA

A:Residues: 1-211 <KIR>

A:Cross-references: UNIPROT:Q9NP95; DBJ:AB044277

C:Comment: This factor is involved in physiological and pathological processes, playing

C:Genetics:

A:Gene: fgf-20

A:Map position: 8p21.3-8p22

C:Superfamily: fibroblast growth factor

C:Keywords: angiogenesis; carcinogenesis

Query Match 14.5%; Score 161; DB 2; Length 211;

Best Local Similarity 33.1%; Pred. No. 9.8e-06;

Matches 53; Conservative 19; Mismatches 64; Indels 24; Gaps 6;

Qy 32 PDSSPLQFGGQVRQRYLYTDDAQTEAHLEIREDTGVGA-ADQSPESLQKALKPGV 90

Db 52 PGAAQLAHLGLIRRLRQLYC----RTGFHLQLPDGVSQGTQRDHSFLGILEFISVAVGL 107

Qy 91 IQILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLEDGYNVQSEAH-----GLPLH 145

Db 108 VSIRGVDSGLYGMNDKELYGSEKLTSE-CIFRQFENWNTYSSNIYKHGDTGRYP 166

Qy 146 LPGNKSHPRDAPRGAPR-----FLPLPLPALPE 176

Db 167 VALNK-----DGTFRGASKRHKQKTHFLPRVDPERVE 202

RESULT 14

JC4627

fibroblast growth factor 3 - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: JC4627

R:Kiefer, P.; Straehle, U.; Dickson, C.

Gene 168, 211-215, 1996

A:Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic organ

A:Reference number: JC4627; MUID:96194899; PMID:8654946

A:Accession: JC4627

A:Molecule type: mRNA

A:Residues: 1-256 <KIB>

A:Cross-references: UNIPROT:P48802; EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g9713

A:Experimental source: embryo

A:Note: The authors translated the codon TGG for residue 178 as His

C:Comment: This factor belongs to the fibroblast growth factor family which have the fun

ction is a cell signalling molecule and plays the roles during the early stages of devel

C:Genetics:

A:Gene: Fgf-3

A:Introns: 93/2; 127/3

C:Superfamily: fibroblast growth factor

C:Keywords: embryo; fibroblast; growth factor

Query Match 14.4%; Score 160.5; DB 2; Length 256;

Best Local Similarity 28.1%; Pred. No. 1.3e-05;

Matches 47; Conservative 22; Mismatches 47; Indels 51; Gaps 5;

Qy 41 GGQVRQRYLYTDDAQTEAHLEIREDTGVGAADQ-SPESLQKALKPGVQIILGVKTS 99

Db 58 GGAPRRRLKLYC----ATKIHQIHPNGKIDGLENNPLSILEITAVDVGVAIKGLPSG 113

Qy 100 RFLCQRPDGLYGLSLHFDPEACSFRELLEDGYNVQSEAHGLPLHLPGNKSPHRDPAPR 159

Db 114 RYLAWNEKGRLYASVFNR-CEFLERIHLEIGYNTYASRHH----- 154

Qy 160 GPAPFLPLGPPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPS 206

Db 155 -----TTQPPPTGSG-----IGSKRRASS 174

RESULT 15

JC7511

fibroblast growth factor-20 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C:Accession: JC7511

R:Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusui, N.; Ibi, T.; Akaike, A.; Itoh, N.

Biochem. Biophys. Res. Commun. 277, 355-360, 2000

A:Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substantia

A:Reference number: JC7511; MUID:20490008; PMID:11032730

A:Contents: Brain

A:Accession: JC7511

A:Molecule type: DNA

A:Residues: 1-212 <OHM>

A:Cross-references: UNIPROT:Q9EST9; DBJ:AB020021

C:Comment: This factor is secreted, and plays an important role as a neurotrophic factor

C:Genetics:

A:Gene: fgf-20

C:Keywords: brain; growth factor; neurotrophic factor

Query Match 14.4%; Score 160; DB 2; Length 212;

Best Local Similarity 33.8%; Pred. No. 1.2e-05;

Matches 54; Conservative 17; Mismatches 65; Indels 24; Gaps 6;

Qy 32 PDSSPLQFGGQVRQRYLYTDDAQTEAHLEIREDTGVGA-ADQSPESLQKALKPGV 90

Db 52 PGVELAHLHLIRRLRQLYC----RTGFHLQLPDGVSQGTQRDHSFLGILEFISVAVGL 107

Qy 91 IQILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLEDGYNVQSEAH-----GLPLH 145

Db 108 VSIRGVDSGLYGMNDKELYGSEKLTSE-CIFRQFENWNTYSSNIYKHGDTGRYP 166

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:54:48 ; Search time 251.671 Seconds
(without alignments)
425.256 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 1113

Sequence: 1 MDSBTGFHSLVWVLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1113	100.0	209	1 FGFL_HUMAN	Q9nsal homo sapien
2	1106	99.4	209	2 Q9N683	Q8h683 homo sapien
3	803.5	72.2	208	2 Q8V180	Q8v180 rattus norv
4	793.5	71.3	210	1 FGFL_MOUSE	Q9j1n1 mus musculus
5	265	23.8	216	1 FGFL_HUMAN	Q95750 homo sapien
6	249.5	22.4	251	1 FGFL_MOUSE	Q8epc2 mus musculus
7	235.5	21.2	251	1 FGFL_RAT	Q8v182 rattus norv
8	222.5	20.0	251	1 FGFL_HUMAN	Q9gzv9 homo sapien
9	216.5	19.5	227	2 Q9DDN0	Q35622 mus musculus
10	206.5	18.6	218	1 FGFL_MOUSE	Q8v181 rattus norv
11	206.5	18.6	218	2 Q8V181	P05524 mus musculus
12	179	16.1	274	1 FGFL_MOUSE	P11487 homo sapien
13	177.5	15.9	239	1 FGFL_HUMAN	P48803 bos taurus
14	177	15.9	206	1 FGFL_BOVIN	Q8axal brachydanio
15	176.5	15.9	205	2 Q8AXA1	P10767 homo sapien
16	176.5	15.9	208	1 FGFL_HUMAN	P48805 xenopus lae
17	174	15.6	187	1 FGFL_XENLA	Q8f515 rattus norv
18	171.5	15.4	208	2 Q8F515	Q8ygd8 oncorhynch
19	171	15.4	206	2 Q8YGD8	Q8c399 mus musculus
20	171	15.4	245	2 Q8R5L9	Q8c399 mus musculus
21	170.5	15.3	195	2 Q8C399	P21658 mus musculus
22	170.5	15.3	208	1 FGFL_MOUSE	Q9yh31 notophthalm
23	168	15.1	196	2 Q9YH31	Q9sel9 mus musculus
24	168	15.1	212	2 Q9SEL9	Q9oxq5 ambystoma m
25	167.5	15.0	124	2 Q9OXQ5	P48807 rattus norv
26	167	15.0	266	1 FGFL_RAT	P48804 gallus gall
27	165	14.8	194	1 FGFL_CHICK	Q8c7a8 mus musculus
28	165	14.8	211	2 Q8C7A8	P15656 mus musculus
29	164	14.7	264	1 FGFL_MOUSE	P48806 xenopus lae
30	163.5	14.7	192	1 FGFL_XENLA	P08620 homo sapien
31	163.5	14.7	206	1 FGFL_HUMAN	

32	163	14.6	87	2 Q76B59	Q76b59 gallus gall
33	162.5	14.6	147	1 FGFL_BRARE	Q6bpt8 brachydanio
34	161	14.5	211	1 FGFL_HUMAN	Q9np95 homo sapien
35	161	14.5	247	1 FGFL_RAT	Q8f517 rattus norv
36	160.5	14.4	256	1 FGFL_BRARE	P48802 brachydanio
37	160	14.4	111	2 Q9OXQ1	Q9oxq1 ambystoma m
38	160	14.4	212	2 Q9EST9	Q9est9 rattus norv
39	159.5	14.3	191	2 Q9DFC9	Q9dfc9 brachydanio
40	159	14.3	237	2 Q9IAI6	Q9iai6 gallus gall
41	159	14.3	247	1 FGFL_HUMAN	Q92915 homo sapien
42	157.5	14.2	208	2 Q7ZZN4	Q7zzn4 gallus gall
43	157.5	14.2	268	2 Q8NF90	Q8nf90 homo sapien
44	157	14.1	208	1 FGFL_HUMAN	P31371 homo sapien
45	157	14.1	208	1 FGFL_RAT	P36364 rattus norv

ALIGNMENTS

RESULT 1

ID	FGFL_HUMAN	STANDARD;	PRT;	209 AA.
AC	Q9NSA1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).			
GN	Name=FGF21;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;			
RA	Nishimura T., Nakatake Y., Konishi M., Itoh N.;			
RT	"Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";			
RL	Biochim. Biophys. Acta 1492:203-206(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;			
RA	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";			
RT	Genome Res. 13:2265-2270(2003).			
RL	[3]			
RP	SEQUENCE OF 29-43.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";			
RL	Protein Sci. 13:2819-2824(2004).			
CC	-!- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-!- SIMILARITY: Belongs to the heparin-binding growth factors family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			

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DR EMBL; AB021975; BAA99415.1; -.
DR EMBL; AY359086; AAQ89444.1; -.
DR HSSP; P03968; 1BAR.
DR Genew; HGNC:3678; FGF21.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFGF.
DR PRINTS; PR00262; ILIHBGF.
DR PRODOM; PD000831; ILI_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE NEG.
KW Direct protein sequencing; Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 209 Fibroblast growth factor-21.
FT CONFLICT 23 23 Missing (in Ref. 2)
FT CONFLICT 23 23 Missing (in Ref. 2)
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 1113; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.4e-72;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIRDGTGVTGGAADQSPESLIQLKALPGVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIRDGTGVTGGAADQSPESLIQLKALPGVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
QY 181 LAQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB 181 LAQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 2
Q8N683 PRELIMINARY; PRT; 209 AA.
AC Q8N683;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21,.
GN Name=FGF21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR EMBL; BC018404; AAH18404.1; -.
DR HSSP; O95750; 1PWA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFGF.
DR PRINTS; PR00262; ILIHBGF.
DR PRODOM; PD000831; ILI_HBGF; 1.
DR SMART; SM00442; FGF; 1.
KW Growth factor.
SQ SEQUENCE 209 AA; 22284 MW; 27925C43B5167823 CRC64;

Query Match 99.4%; Score 1106; DB 2; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.6e-72;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIRDGTGVTGGAADQSPESLIQLKALPGVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIRDGTGVTGGAADQSPESLIQLKALPGVIQLGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
QY 181 LAQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB 181 LAQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 3
Q8VI80 PRELIMINARY; PRT; 208 AA.
AC Q8VI80;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
GN Name=FGF21;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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DR SMART: SM00442; FGF, 1.
KW Growth factor.
SQ SEQUENCE 208 AA; 22857 MW; D232445902CDB9EA CRC64;
Query Match 72.2%; Score 803.5; DB 2; Length 208;
Best Local Similarity 78.9%; Pred. No. 2.8e-50;
Matches 157; Conservative 12; Mismatches 27; Indels 3; Gaps 2;
QY 12 GLWVSVLGL-LIGACQAHPIPDSSPLQFGQVQRVRYLYTDDAQTEAHLREIDGTGVG 70
DB 12 GLWVCLLVFLVGLGVEAYPIPDSSPLQFGQVQRVRYLYTDDQTEAHLREIDGTGV 71
QY 71 GAADSPESLLOLKALPKGVQIQLGVKTSRFLCORPDGALYGLSLHDPDCACSFRELLLED 130
DB 72 GTARSPESLLELKALPKGVQIQLGVKTSRFLCORPDGALYGLSLHDPDCACSFRELLLED 131
QY 131 GYNVQSEAHGLPLHLPGNKNKSPHDPAPRGPARFLPLGLPALPEPPCGLAPQPPDVGS 190
DB 132 GYNVQSEAHGLPLHLPGNKNKSPHDPAPRGPARFLPLGLPALPEPPCGLAPQPPDVGS 189
QY 191 SDPLSNVQSGRSPSYAS 209
DB 190 SDPLSNVQSGRSPSYAS 208
RESULT 4
ID FGFL MOUSE STANDARD; PRT; 210 AA.
AC Q9JUN1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21).
GN Name=FGF21;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
RT the liver";
RL Biochim. Biophys. Acta 1492:203-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ighii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC 1- SUBCELLULAR LOCATION: Secreted (Potential).
CC 1- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also
CC expressed in the thymus at lower levels.
CC 1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB025718; BAA99416.1; -;
CC EMBL; AK007574; BAB25115.1; -;
CC EMBL; BC049592; AHA49592.1; -;
CC HSSP; P08620; 11JT.
CC MGD; MGI:1861377; Fgf21.
CC InterPro; IPR008996; Cytok_IL1_like.
CC InterPro; IPR002209; HB/F_growthfact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGF_FGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 210 Fibroblast growth factor-21.
SQ SEQUENCE 210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;
Query Match 71.3%; Score 793.5; DB 1; Length 210;
Best Local Similarity 78.9%; Pred. No. 1.5e-49;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;
QY 12 GLWVS-VLAGLLIGACQAHPIPDSSPLQFGQVQRVRYLYTDDAQTEAHLREIDGTGVG 70
DB 12 GLWVRLLVFLVGLGVEAYPIPDSSPLQFGQVQRVRYLYTDDQTEAHLREIDGTGV 71
QY 71 GAADSPESLLOLKALPKGVQIQLGVKTSRFLCORPDGALYGLSLHDPDCACSFRELLLED 130
DB 72 GAARSPESLLELKALPKGVQIQLGVKTSRFLCORPDGALYGLSLHDPDCACSFRELLLED 131

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OY 131 GYNYVQSAHGLPLHLGNKSPHRDPAPRGPARFLPLGLPALPPEPPGILAPOPPDVG 190
DB 132 GYNYVQSAHGLPLHLGNKSPHRDPAPRGPARFLPLGLPALPPEPPGILAPOPPDVG 191
OY 191 SDPLSMVQSPQGRSPSYAS 209
DB 192 SDPLSMVQSPQGRSPSYAS 210

RESULT 5
ID_FGFJ_HUMAN STANDARD; PRT; 216 AA.
AC O95750.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Fibroblast growth factor-19 precursor (FGF-19) (UNQ334/PRO533).
GN Name=FGF19;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99132028; PubMed=9931477; DOI=10.1016/S0167-4781(98)00255-3;
RA Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
RT "Structure and expression of a novel human FGF, FGF-19, expressed in
RL the fetal brain.";
RL Biochim. Biophys. Acta 1444:148-151(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,
RA Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A.,
RA Gurney A.L.;
RT "FGF-19, a novel fibroblast growth factor with unique specificity for
RT FGFR4";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242638999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeney R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: May be involved in brain development during
CC embryogenesis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed only in fetal brain.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
DR EMBL; AB018122; BAA75500.1; -
DR EMBL; AF110400; AAD45973.1; -
DR EMBL; AY358302; AAO88669.1; -
DR EMBL; BT006729; AAP35375.1; -
DR EMBL; BC017664; AAI17664.1; -
DR FDB; IPWA; X-ray; A=35-196.
DR Genew; HGNC:3675; FGF19.
DR H-InvDB; HIX0009891; -
DR MIM; 603891; -
DR GO; GO:0007399; P-neurogenesis; TAS.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F_GrowthFact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFHGF.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD008831; IL1_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW 3D-structure; Direct protein sequencing; Growth factor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 216 Fibroblast growth factor-19.
SQ SEQUENCE 216 AA; 24002 MW; E0BCBC9C220F9832 CRC64;
Query Match 23.8%; Score 265; DB 1; Length 216;
Best Local Similarity 36.3%; Pred. No. 1.8e-11;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;
OY 11 SGLVSVVLGILLGACQAHPIPDSSPLLQP--GGQVRQRYLYTDDAQ--QTEAHLEIRDG 67
DB 14 AGLWLAV--AGRPLA-----FSDAGPHVYGVGDPRLRLHLYTSGPHCLSCFLIRADG 66
OY 68 TVGGAADQSPESLLQLKALKEGVIIQLGVKTSRFLQCPDQALYGSLLHFDPEACSFRELL 127
DB 67 VVDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLCMGADGKMGQGLLYQYSEDCAFEBEI 126
OY 128 LEDGVNIVQSAHGLPLHLGNKSPHRDPAPRGPARFLPLGLPALP-----EPPGI--- 180
DB 127 RPDGVNIVYRSEKRLPLVSLSSAKQ--RQLYKNRG---FLPLSHFLPLMPVPEEDLRGH 182
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QY 181 ----LAQPPDVGVSSDPLSMV-GPQGRSPSY 207
Db 183 LRSMDPSSPLETDSMDPGLVGLTGLRAVRSPSF 214

RESULT 6
FCFN MOUSE
ID FCFN MOUSE STANDARD; PRT; 251 AA.
AC Q9BPC2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23).
GN Name=Fgf23;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20490027; PubMed=11032749; DOI=10.1006/bbrc.2000.3696;
RA Yamashita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the brain.";
RT Biochem. Biophys. Res. Commun. 277:494-498 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Embryo;
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.B., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-DePiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23.";
RT Nat. Genet. 26:345-348 (2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Mainly expressed in the brain and thymus at low levels. In brain; preferentially expressed in the ventrolateral thalamic nucleus.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC
CC EMBL; AB037889; BAB13478.1; -
CC EMBL; AF263536; AAG09916.1; -
CC PIR; JC7513; JC7513.
CC HSSP; P03968; 1BAR.
CC MGD; MGI:1891427; Fgf23.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 251 Fibroblast growth factor-23.
SQ SEQUENCE 251 AA; 27757 MW; 110C1F2C735DC360 CRC64;

Query Match 22.4%; Score 249.5; DB 1; Length 251;
Best Local Similarity 35.1%; Pred. No. 2.7e-10;
Matches 73; Conservative 27; Mismatches 85; Indels 23; Gaps 8;

QY 12 GLWVSLVGLLIGACQ---AHPIPDSSPLL---QFGQVQRQRYLYTDDAQQTAEHLREID 66
Db 3 GTCLRLVGLVLCVCSLGTARAYPDTSPLLGSNWGSLT---HLXTATA-RTSYHLQIHRD 58

RESULT 7
FCFN RAT
ID FCFN RAT STANDARD; PRT; 251 AA.
AC Q8V1B2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23).
GN Name=Fgf23;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Rattus norvegicus fgf23.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC
CC EMBL; AB078777; BAB84108.1; -
CC HSSP; P03968; 1BAR.
CC RGD; 620178; Fgf23.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 251 Fibroblast growth factor-23.
SQ SEQUENCE 251 AA; 27911 MW; 35A229E1B3900593 CRC64;

Query Match 21.2%; Score 235.5; DB 1; Length 251;
Best Local Similarity 34.1%; Pred. No. 2.8e-09;
Matches 71; Conservative 28; Mismatches 86; Indels 23; Gaps 8;

QY 12 GLWVSLVGLLIGACQ---AHPIPDSSPLL---QFGQVQRQRYLYTDDAQQTAEHLREID 66
Db 3 GACRLLVGLVLCVCSLGTARAYSDTSPLLGSNWGSLT---HLXTATARN-S-YHLQIHRD 58

QY 67 GTVGAADQSPESLLQLKALPGVVIQLGVKTSRFLCORPDGALYGLSHLFDPEACSFREL 126
Db 59 GHVDGTPHQITYSALMITSEDAGSVIIGAMTRRFLCMLDHLGNIFGSLHFSPEACKFRQW 118

QY 127 LLEDGVNVYQSEANGLPLHLPGNK---SPHRDPAPRGAPREL-----PLPGLPALPEP 177
Db 119 TLENGYDVYLSQKHLYSLGRKRIFOGNTNPPPF--SQFLARNEVPLLHFTYTRPRR 176

QY 178 PGILAPQPPDVGVSSDPLSMVGPSPQGRSP 205
Db 177 HTRSADPE---RDPLNVLKRPRATP 201
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QY 178 FGLAPQPPDVGVSSDPLSMVGPQGRSP 205
Db 177 HTRSEDPEP---RDPLNVLKPRPRATP 201

RESULT 8
FCFN HUMAN
ID_FCN HUMAN STANDARD; PRT; 251 AA.
AC Q9GZV9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23) (Tumor-derived
DE hypophosphatemia inducing factor) (UNQ3027/PRO9828).
GN Name=FGF23; Synonyms=HYFP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20490027; PubMed=11032749; DOI=10.1006/bbrc.2000.3696;
RA Yamashita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23,
RT preferentially expressed in the ventrolateral thalamic nucleus of the
RT brain.";
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A., VARIANTS ADHR GLN-176; GLN-179 AND TRP-179, AND
RP VARIANT MET-239.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA Lorenz-DePiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with
RT mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21267444; PubMed=11344269; DOI=10.1073/pnas.101545198;
RA Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takeda S.,
RA Takeuchi Y., Fujita T., Fukumoto S., Yamashita T.;
RT "Cloning and characterization of FGF23 as a causative factor of tumor-
RT induced osteomalacia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS SER-195 AND MET-239.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.D., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RT "NIHES-SNP6, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally

RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -|- SUBCELLULAR LOCATION: Secreted (Potential).
CC -|- DISEASE: Defects in FGF23 are the cause of autosomal dominant
CC hypophosphataemic rickets (ADHR) [MIM:193100]. ADHR is
CC characterized by low serum phosphorus concentrations, rickets,
CC osteomalacia, leg deformities, short stature, bone pain and dental
CC abscesses.
CC -|- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
CC EMBL; AB037973; BAB13477.1; -;
CC EMBL; AF263537; AAG09917.1; -;
CC EMBL; AB047858; BAB55889.1; -;
CC EMBL; AY358323; AAG88689.1; -;
CC EMBL; AY566236; AAS9157.1; -;
CC HSSP; Q02195; 100K.
CC Genew; HGNC:3680; FGF23.
CC MIM; 605380; -;
CC MIM; 193100; -;
CC GO; GO:0005615; C:extracellular space; NAS.
CC GO; GO:0030154; P:cell differentiation; NAS.
CC InterPro; IPR008996; Cytok IL1-like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF_1
CC PRINTS; PR00262; ILHBGF.
CC PRODOM; PD000831; IL1_HBGF; 1.
CC PROSITE; PS00247; HBGF_FGF; FALSE NEG.
CC KW Direct protein sequencing; Disease mutation; Growth factor;
KW Polymorphism; Signal.
FT SIGNAL 1 24
FT CHAIN 25 251 Fibroblast growth factor-23.
FT VARIANT 176 176 R -> Q (in ADHR).
FT FTID=VAR_010717.
FT R -> Q (in ADHR).
FT FTID=VAR_010719.
FT R -> W (in ADHR).
FT FTID=VAR_010718.
FT P -> S.
FT FTID=VAR_018887.
FT T -> M (in dBSNP:7955866).
FT FTID=VAR_010720.
FT SQ SEQUENCE 251 AA; 27954 MW; 6093BD0CC50C2489 CRC64;
Query Match 20.0%; Score 222.5; DB 1; Length 251;
Best Local Similarity 30.8%; Pred. No. 2.4e-08;
Matches 68; Conservative 36; Mismatches 70; Indels 47; Gaps 9;
QY 13 LMVSVLAGLL-LGACQAHPIPDSSPLL--OPFGOVQRQRYLYTDDAQOTEAHLETRDQTV 69
Db 8 LMVCAVCVCSMSVLRAY--PNASPLGSSWGGLI---HLTATARN--YHLQHKHGHV 61
QY 70 GGAADQSPESLLQALKKPGVQIQLGVKTSRFLCORPDGALYGLSLHFDPEACSFRELLLE 129
Db 62 DGAPHQTIYSALMIRSEDAQFPVITGVMSRYLWDFRGNIFGSHYFPDPCRFQHOTLE 121
QY 130 DGYNVYQSEAGHLPLHLPGNKSPHRDPAPRGPAPFLPLGPPALPEPP----- 178
Db 122 NGYDVTHSPQVHFLVSL-----GRAKRAFLPGMNP-----PPYSQFLSRNEI 164
QY 179 ---GLAPQP-----PDVGSDDLPLSMVGPQGRSPSYAS 209
Db 165 PLIHFTPIPRHTRSAEDDSERDPLNVLKPRARMTAPAS 205
RESULT 9


```
Q9DDNO
ID Q9DDNO PRELIMINARY; PRT; 227 AA.
AC Q9DDNO;
DT 01-WAR-2001 (TRENBLrel. 16, Created)
DT 01-WAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibroblast growth factor 19.
GN Name=fgf-19;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20564778; PubMed=11110663; DOI=10.1126/science.290.5498.1965;
RA Lader R.K., Anake K.U., Gurney A.L., Schoenwolf G.C.,
RA Francis-West P.H.;
RT "Identification of synergistic signals initiating inner ear
RT development.";
RL Science 290:1965-1967(2000).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR EMBL; AF315355; AAG39478.1; -.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR InterPro; IPR008996; Cycok_IL1_like.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
KW Growth factor.
SQ SEQUENCE 227 AA; 24568 MW; 875D76FBFD09F8E2 CRC64;

Query Match 19.5%; Score 216.5; DB 2; Length 227;
Best Local Similarity 30.9%; Pred. No. 5.8e-08;
Matches 67; Conservative 33; Mismatches 84; Indels 33; Gaps 10;

Qy 18 LAGLLGACQAH--PIPD-SSPLLOFG-QQ-VQRVLYTDDAQ--TEAHLEIRDGTVG 70
Db 15 LGTAAARAAARSLPDPVGGPHVNGCEPIRLHLLHRPGKGLGFCFLRIGDGRVD 74
Qy 71 GAADQSPSLQLKALKEGVILQGVKTSRFLCQRPDGCALYGLSLHFDPEACSFRELLLED 130
Db 75 AVGSQSPQLLEIRAVAVRTVAIKGVQSSRYLCWDEAGRLHGQLSYSDCSFEEIRPD 134
Qy 131 GYNVYQSEAHGLPLHLGNKSPH-----RDPAPRGPARFLPLPLPPA----- 173
Db 135 GYNVYKSKYKIGTSVSLSSAKORQPKGKDFLPL--SHFLPMINTVPVVEVTFDGEYDYSQ 192
Qy 174 --LPEPPGILAPQPDVGSPPSLMVGP--SQGRSPSY 207
Db 193 AFEPE-----VYSSPLETSDMPFGITSKLSPVKSPSF 225

RESULT 10
FGFF_MOUSE
ID FGFF_MOUSE STANDARD; PRT; 218 AA.
AC Q35622;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-15 precursor (FGF-15).
GN Name=fgf15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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```
RX MEDLINE=97454242; PubMed=9310317;
RA McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.;
RT "A novel fibroblast growth factor gene expressed in the developing
RT nervous system is a downstream target of the chimeric homeodomain
RT oncoprotein E2A-Pbx1.";
RL Development 124:3221-3232(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
RA Nikaido I., Oeato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havaehizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play an important role in regulating cell division
CC and patterning within specific regions of the embryonic brain,
CC spinal cord and sensory organs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
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DR EMBL; AF007268; BAB3197.1; -;
DR EMBL; AK017829; BAB30961.1; -;
DR EMBL; BC021328; AAH21328.1; -;
DR HSSP; Q02195; LQOK.
DR MGD; MGI:1096383; Fgf15.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1_HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 218 Fibroblast growth factor-15.
SQ SEQUENCE 218 AA; 25236 MW; A96B0D771FE125A5 CRC64;

Query Match 18.6%; Score 206.5; DB 1; Length 218;
Best Local Similarity 33.8%; Pred. No. 2.9e-07;
Matches 53; Conservative 29; Mismatches 70; Indels 5; Gaps 4;

QY 13 LWSVLAGLLGACQAHPIPDSSPLQFG-GGV-RQRYLYTDDAQOQTEAHLEIREDGTVG 70
DB 19 LMLAVSGRPL--AQOSQVSDEBPLFLYWGKITRLQLYSAGPYVSNCFILRISDGSVD 76
QY 71 GAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGLYGLSHLFDPEACSFRELLLED 130
DB 77 CEEDQNERNLLEFRAVALKTAIKDVSSVRYLCSADGKIYGLIRYSEEDCTFREMDCL 136
QY 131 GYNYQSEAHGLPLHLPGNKS-PHRDPAPRGPAPFLPL 167
DB 137 GYNQYRSMKHLHIIIFIQAK-PREQLQDQKPSNFIPV 172

RESULT 11
QYBI81
ID Q8VI81 PRELIMINARY; PRT; 218 AA.
AC Q8VI81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 15.
GN Name=FGF15;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078900; BAB24298.1; -;
DR HSSP; Q95750; IPWA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1_HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 218 AA; 25207 MW; ED986864B5307C58 CRC64;

Query Match 18.6%; Score 206.5; DB 2; Length 218;
Best Local Similarity 30.7%; Pred. No. 2.9e-07;
Matches 62; Conservative 37; Mismatches 92; Indels 11; Gaps 7;

QY 13 LWSVLAGLLGACQAHPIPDSSPLQFG-GGV-RQRYLYTDDAQOQTEAHLEIREDGTVG 70
DB 19 LMLAVSGRPLVQ--QSQSVSDGEGPLFLYWGKITRLQLYSAGPYVSNCFILRISDGSVD 76

QY 71 GAADQSPESLLQKALKPGVQILGVKTSRFLCQRPDGLYGLSHLFDPEACSFRELLLED 130
DB 77 CEEDQNERNLLEFRAVALKTAIKDVSSVRYLCSADGKIYGLIRYSEEDCTFREMDCL 136
QY 131 GYNYQSEAHGLPLHLPGNKS-PHRDPAPRGPAPFLPL--PGLPALPPEPPGILAPQPPD 187
DB 137 GYNQYRSMKHLHIIIFIQAKPREQLQDQKPSNFIPFHRSPPFESTDQLRSKMFLSPLPLE 194
QY 188 VGSDPPLSMVGPSQG--RSPSY 207
DB 195 SDSMDPFRMVEDVDHLVKSPSF 216

RESULT 12

ID FGF3_MOUSE STANDARD; PRT; 274 AA.
AC P05524; Q61736;
DT 01-NOV-1988 (Rel. 09, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
GN Name=Fgf3; Synonyms=Fgf-3, Int-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), ALTERNATIVE INITIATION,
RP SUBCELLULAR LOCATION, AND MUTAGENESIS OF ASN-94.
RA MEDLINE=90158795; PubMed=2406607; DOI=10.1038/343662a0;
RX Acland P., Dixon M., Peters G., Dickson C.;
RT "Subcellular face of the int-2 oncoprotein is determined by choice of
RT initiation codon.";
RL Nature 343:662-665(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus.";
RL EMO J. 5:919-924(1986).
RN [3]
RP SEQUENCE OF 1-102 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal
RT carcinoma cell lines encode a protein with homology to fibroblast
RT growth factors.";
RL EMO J. 7:1013-1022(1988).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA Walther W., Fuller-Pace F., Klefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor
RT family.";
RL J. Cell Sci. Suppl. 13:87-96(1990).
CC -!- FUNCTION: Could be involved in ear development.
CC -!- SUBCELLULAR LOCATION: Nucleus (isoform 1). Endoplasmic reticulum
CC and Golgi (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative initiation;
CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC alternative initiation. Isoform 1 starts at an alternative CUG
CC codon;
CC -!- INDUCTION: By integration of mouse mammary tumor virus.
CC -!- PTM: Glycosylated.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.

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DR EMBL; X52014; CAA36261.1; -
DR EMBL; Y00848; CAA68767.1; ALT_INIT.
DR FIR; A23930; TWMSY2.
DR HSSP; O15520; INUN.
DR MGI; 95517; Fgf3.
DR GO; 0001759; P:induction of an organ; IMP.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F_Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Alternative initiation; Glycoprotein; Growth factor; Mitogen;
KW Nuclear protein; Proto-oncogene; Signal.
FT CHAIN 1 274 INT-2 proto-oncogene protein, isoform 1.
FT SIGNAL 30 46 Potential, isoform 2.
FT CHAIN 47 274 INT-2 proto-oncogene protein, isoform 2.
FT INIT MET 30 30 For isoform 2.
FT CARBOHYD 94 94 N-linked (GlcNAc...)
FT MUTAGEN 94 94 N->Q: Not glycosylated.
SQ SEQUENCE 274 AA; 30072 MW; 6A245C9D6FC9AE3 CRC64;

Query Match 16.1%; Score 179; DB 1; Length 274;
Best Local Similarity 28.8%; Pred. No. 3.6e-05;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;
QY 41 GGVQRVLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVIOILGVKTSR 100
DB 69 GGAPRRRLKLYC-----ATKYLQLHPSGRVNGSLNSAYSILITAVEGVIAIKGLFSGR 124
QY 101 FLCORPDGALVSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSP--HRDPAP 158
DB 125 YLAMNKRGLYASDHVNAE-CFVERIHELGINTYASR-----LYRTSGSGGAGRQPCA 178
QY 159 RGP-----ARFLPLGLPALPEPPGILAPDDVGSSDPLSMVGPSPGSPFVAS 209
DB 179 QRPWTVSVNGKGRPRGRGFKTRRTQKSLFLPVLGHKDHMVRLQLQSQPRAPGEGS 235

RESULT 13
FGF3_HUMAN STANDARD; PRT; 239 AA.
AC P11487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
GN Name=FGF3; Synonyms=INT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89239468; PubMed=2470007;
RA Brooks S., Smith R., Casey G., Dickson C., Peters G.;
RT "Sequence organization of the human int-2 gene and its expression in
RL teratocarcinoma cells."
RL Oncogene 4:429-436(1989).
CC -!- FUNCTION: Could be involved in ear development.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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DR EMBL; X14445; CAA32615.1; -
DR FIR; S04742; S04742.
DR HSSP; O15520; INUN.
DR Genew; HGNC:3681; FGF3.
DR MIM; 164950; -
DR GO; 0005576; C:extracellular; TAS.
DR GO; 0008083; P:growth factor activity; TAS.
DR GO; 0007267; P:cell-cell signaling; TAS.
DR GO; 0009653; P:morphogenesis; TAS.
DR GO; 0007165; P:signal transduction; TAS.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR002209; HB/F_Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR ProDom; PD000831; IL1_HBGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Glycoprotein; Growth factor; Mitogen; Proto-oncogene; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 239 INT-2 proto-oncogene protein.
FT CARBOHYD 65 65 N-linked (GlcNAc...)(Potential).
SQ SEQUENCE 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;

Query Match 15.9%; Score 177.5; DB 1; Length 239;
Best Local Similarity 29.7%; Pred. No. 4e-05;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GGVQRVLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVIOILGVKTSR 100
DB 40 GGAPRRRLKLYC-----ATKYLQLHPSGRVNGSLNSAYSILITAVEGVIAIKGLFSGR 95
QY 101 FLCORPDGALVSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
DB 96 YLAMNKRGLYASDHVNAE-CFVERIHELGINTYASRILYRTVSTTPGAR---RQPSABR 151
QY 159 -----RGPAP-----FLP-----LFLPPLPEPPG 179
DB 152 LWYTVSVNGKGRPRGRGFKTRRTQKSLFLPVLGHKDHMVRLQLQSQPRPPG 203

RESULT 14
FGF4_BOVIN STANDARD; PRT; 206 AA.
ID FGF4_BOVIN STANDARD; PRT; 206 AA.
AC P48503;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST) (HBGF-4).
GN Name=FGF4; Synonyms=HST;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=96032369; PubMed=7557455; DOI=10.1016/0378-1119(95)00330-9;
RA Yu J.C., Desseabra A.J., Wang L.M., Fleming T.P., Chedid M., Miki T.,
RA Heidaran M.A.;
RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine
RT hst.";
RL Gene 162:333-334(1995).

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CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC -----
CC EMBL; U15969; AAA91622.1; -
CC HSP; P08620; 11UT.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002209; HB/F_growthfact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGF_FGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor; Mitogen; Proto-oncogene; Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 206 Fibroblast growth factor-4.
SQ SEQUENCE 206 AA; 22041 MW; F9B7A8606E56613 CRC64;

Query Match 15.9%; Score 177; DB 1; Length 206;
Best Local Similarity 32.1%; Pred. No. 3.7e-05;
Matches 52; Conservative 23; Mismatches 75; Indels 12; Gaps 5;

QY 14 WSVVLGALLGACQAHPIPDSSPLLQFGQV-----RORYLYTDDAQQTEAHLEIREDTG 68
DB 46 WESLVARSLLAGLPVAAQPKAAVOSGAGDYLLGKRLRLRYCNVG--IGFHLQVLDPGR 103

QY 69 VCGAADQPESLLQALKKPGVIQILGVKTSRFLCQPDGALYGLSLHFDPEACSPRELL 128
DB 104 IGGVHADTSDSLLLESPVERGVSVTFVARSFFVAMSSRGRLYSGSPFTDE-CRPREILL 162

QY 129 EDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
DB 163 PNNYNAYECDRHPCGFIALSKNGKAKGNRVSPTMKVTHFLP 204

RESULT 15
Q8AXA1 PRELIMINARY; PRT; 205 AA.
ID Q8AXA1;
AC Q8AXA1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibroblast growth factor 6.
GN Name=fgf6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ralliere C., Rescan P.-Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC EMBL; AF516334; AAO15997.1; -.
CC HSP; P08620; 11UT.
CC ZFIN; ZDB-GENE-980526-559; fgf6.
CC GO; GO:0008083; F: growth factor activity; IEA.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR002209; HB/F_growthfact.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00263; HBGF_FGF.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
```

```
DR SMART: SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor.
SQ SEQUENCE 205 AA; 23244 MW; 2BDB1D93D6533696 CRC64;

Query Match 15.9%; Score 176.5; DB 2; Length 205;
Best Local Similarity 28.4%; Pred. No. 4e-05;
Matches 56; Conservative 26; Mismatches 70; Indels 45; Gaps 7;

QY 9 EHSGLW---VSVLAGLLGACQAHPIPD----- 33
DB 13 ESSGRWTWTAVVLGFLGIVSSYPTSDRTNATSLKKRWKLPGRSVLGISVEKSDLNWE 72

QY 34 SSPLLQFGQVQRORYLYTDDAQQTEAHLEIREDTGTVCGAADQSPESLLQALKKPGVIQI 93
DB 73 SDYLL---GIKRVRLRYCNVG--IGFHLQVLDPGRINGVHNENQYSLIEISAVRGGVSL 127

QY 94 LGVKTSRFLCQPDGALYGLSLHFDPEACSFRELLEDGYNVYQSEAH-GLPLHLPGN--- 149
DB 128 YGVASGLFVAMSSRGRLYGTAFRDE-CKFKETLLPNNYNAYESSIYKGYFYMALSKHGRL 186

QY 150 KSPHRDPAPRGPARFLP 166
DB 187 KRGRASPAMTVTHFLP 203
```

Search completed: July 8, 2005, 22:18:01
Job time : 252.671 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:53:57 ; Search time 20.9333 Seconds
(without alignments)
295.613 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 KQRYLYTDDAQOQTEAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	4	AAB68418
2	86	100.0	91	8	ADL57115
3	86	100.0	124	5	ABB81312
4	86	100.0	125	8	ADL57107
5	86	100.0	153	4	AB73069
6	86	100.0	181	4	AU00965
7	86	100.0	183	8	ADL57109
8	86	100.0	208	4	AAE05078
9	86	100.0	208	5	AAU83630
10	86	100.0	208	5	ABG32358
11	86	100.0	208	5	AAE17601
12	86	100.0	208	6	ABU80777
13	86	100.0	208	6	ABO33743
14	86	100.0	208	6	ABU82086
15	86	100.0	208	6	ABP96156
16	86	100.0	208	6	ABJ72366
17	86	100.0	208	6	ABJ72394
18	86	100.0	208	6	ABO34289
19	86	100.0	208	7	ADA37038
20	86	100.0	208	7	ABJ72096
21	86	100.0	208	7	ADB83568
22	86	100.0	208	7	ADB80674
23	86	100.0	208	7	ADB73215
24	86	100.0	208	7	ADB78297
25	86	100.0	208	7	ADB84945

26	86	100.0	208	7	ADB78051	Novel hum
27	86	100.0	208	7	ADB87117	Human PRO
28	86	100.0	208	7	ADB84699	Human PRO
29	86	100.0	208	7	ADB83814	Novel hum
30	86	100.0	208	7	ADB72969	Novel hum
31	86	100.0	208	7	ADC36807	Human PRO
32	86	100.0	208	7	ADC21797	Human PRO
33	86	100.0	208	7	ADC49828	Novel hum
34	86	100.0	208	7	ADC49027	Novel hum
35	86	100.0	208	7	ADC49544	Novel hum
36	86	100.0	208	7	ADC47405	Novel hum
37	86	100.0	208	7	ADC47150	Novel hum
38	86	100.0	208	7	ADC78025	Novel hum
39	86	100.0	208	7	ADD06260	Novel hum
40	86	100.0	208	7	ADC77779	Novel hum
41	86	100.0	208	7	ADD50742	Novel hum
42	86	100.0	208	7	ADD50988	Novel hum
43	86	100.0	208	7	ADD50469	Human PRO
44	86	100.0	208	7	ADD50223	Human PRO
45	86	100.0	208	7	ADD51234	Novel hum

ALIGNMENTS

RESULT 1

AAB68418
ID AAB68418 standard; peptide; 16 AA.

AC AAB68418;

DT 23-JUL-2001 (first entry)

DE Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21).

KW Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

OS Homo sapiens.

PN WO200136640-A2.

PD 25-MAY-2001.

PF 16-NOV-2000; 2000WO-US031745.

PR 18-NOV-1999; 99US-0166540P.

PR 11-MAY-2000; 2000US-0203633P.

(CHIR) CHIRON CORP.

(KYOU) UNIV KYOTO.

PI Itoh N, Kavanagh WM;

WP1; 2001-343823/36.

New nucleic acid molecule useful for treating disease, e.g. infertility, impotence, or testicular cancer.

Claim 17; Page 39; 61pp; English.

The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16
 DB 1 RQRYLYTDDAQQTAAH 16

RESULT 2
 ADLS7115
 ID ADLS7115 standard; protein; 91 AA.
 AC ADLS7115;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human NOV6d protein SEQ ID NO:60.
 XX
 KW human; antidiabetic; anorectic; cardiant; hypotensive;
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
 KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
 KW dermatological; antiasthmatic; antilipaeamic; gene therapy;
 KW fibroblast growth factor receptor 4; FGFR4;
 KW complement factor I precursor; matrix metalloproteinase-15 precursor;
 KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
 KW fibroblast growth factor-21; FGF-21;
 KW alpha-2 macroglobulin-like polypeptide variant;
 KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
 KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
 XX
 OS Homo sapiens.
 XX
 XX WO2004022723-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028141.
 XX
 PR 09-SEP-2002; 2002US-0409145P.
 PR 10-SEP-2002; 2002US-0409544P.
 PR 12-SEP-2002; 2002US-0410320P.
 PR 16-SEP-2002; 2002US-0411060P.
 PR 23-SEP-2002; 2002US-0412768P.
 PR 23-SEP-2002; 2002US-0412825P.
 PR 24-SEP-2002; 2002US-0412767P.
 PR 25-SEP-2002; 2002US-0413342P.
 PR 30-SEP-2002; 2002US-0414832P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
 XX WPI; 2004-315567/29.
 DR N-PSDB; ADLS7114.
 DR
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 XX
 FS Claim 1; SEQ ID NO 60; 214pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX) comprising a
 CC mature form of any of the 37 amino acid sequences fully defined in the
 CC specification. A polypeptide of the invention has antidiabetic,
 CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
 CC virucide, antibacterial, fungicide, protozoacide, nootropic,
 CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
 CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
 CC antilipaeamic activity. A polynucleotide of the invention may have a use
 CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies

are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders (osteoarthritis), haematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidaemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The NOVX polypeptides of the invention show homology to certain known human proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4 (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a shows homology to matrix metalloproteinase-15 precursor; NOV4a shows homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21 (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1 precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology to nuclear hormone receptor NOR-1; NOV11a-11j show homology to transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin-dynorphin precursor. The present sequence represents a NOVX polypeptide of the invention.

Sequence 91 AA;
 Query Match 100.0%; Score 86; DB 8; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16
 DB 45 RQRYLYTDDAQQTAAH 60

RESULT 3
 ABB81312
 ID ABB81312 standard; protein; 124 AA.
 XX
 AC ABB81312;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Human FGF21 core structure amino acid sequence.
 XX
 KW Fibroblast growth factor 9; FGF-9; cytostatic; vulnery; osteopathic;
 KW antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder;
 KW fibroblast growth factor receptor; cancer; bone fracture healing;
 KW bone growth; wound healing; achondroplasia; hypochondroplasia;
 KW osteoporosis; cartilage defect; multiple myeloma.
 XX
 OS Homo sapiens.
 XX
 XX WO200236732-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 18-OCT-2001; 2001WO-IL000962.
 XX
 PR 31-OCT-2000; 2000IL-00139380.
 XX
 PA (PROC-) PROCHON BIOTECH LTD.
 XX
 PI Bogin O, Adar R, Yayon A;
 XX WPI; 2002-479754/51.
 DR

XX New variants of fibroblast growth factor, useful for treating skeletal
PT disorders including osteoporosis, malignancies and to enhance wound and
PT fracture healing.
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC The present invention describes an active variant (I) of a fibroblast
CC growth factor (FGF) having at least one mutation in the beta-8-beta-9
CC loop, having enhanced specificity for one receptor subtype compared to
CC the corresponding wild type FGF, by decreasing the biological activity
CC mediated by at least one receptor subtype while retaining the activity
CC mediated through another receptor subtype. (I) has cytostatic, vulnerary,
CC osteopathic and antiarthritic activities. (I) can be used as a regulator
CC of vasculogenesis or angiogenesis. (I) is useful for preparing a
CC medicament for treating a disease or disorder related to normal or
CC abnormal FGF receptors (FGFRs), especially skeletal disorders, cancer, to
CC enhance bone fracture healing or bone growth processes and wound healing
CC processes. (I) is useful in detection and treatment of various FGFR
CC related disorders including skeletal disorders e.g. achondroplasia,
CC myeloma, epithelial cancers such as transitional cell carcinoma of the
CC bladder and cervical carcinoma. The novel mutants are useful in high
CC expression systems suitable for pharmaceutical production, targeting of
CC drugs or other agents to tissues and cells having specific FGFR subtypes,
CC and serve as template for the formation of improved agonists and
CC antagonists of FGFRs in various disorders such as skeletal disorders and
CC cancer. The present sequence represents a FGF core structure amino acid
CC sequence which is given in the exemplification of the present invention
XX
SQ Sequence 124 AA;
Query Match 100.0%; Score 86; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
DB 1 RQRYLYTDDAQQTAAH 16
RESULT 4
ADL57107
ID ADL57107 standard; protein; 125 AA.
XX
AC ADL57107;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOV5c protein SEQ ID NO:52.
XX
KW human; antidiabetic; anorectic; cardiant; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX
OS Homo sapiens.
XX
FN WO2004022723-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-US028141.
XX
PR 09-SEP-2002; 2002US-0409145P.

PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX (CURA-) CURAGEN CORP.
PI Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
XX WPI; 2004-315567/29.
DR N-PSDB; ADL57106.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1; SEQ ID NO 52; 214pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, and
CC antiarthritic, antiinflammatory, dermatological, antiparasitic, and
CC antilipemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-1lj show homology to
CC transmembrane protein-like; NOV12a-1zc show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
SQ Sequence 125 AA;
Query Match 100.0%; Score 86; DB 8; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
DB 17 RQRYLYTDDAQQTAAH 32

RESULT 5
 ID AAB73069 standard; protein; 153 AA.
 AC AAB73069;
 DT 17-MAY-2001 (first entry)
 XX Human fibroblast growth factor 19 homologue FGF19X.
 DE Human; fibroblast growth factor 19; FGF19X; embryonic development;
 KW proliferative disorder; cancer; restenosis; psoriasis;
 KW rheumatoid arthritis; Dupuytren's contracture.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200118209-A1.
 PD 15-MAR-2001.
 XX 08-SEP-2000; 2000WO-US024863.
 PF 10-SEP-1999; 99US-0153303P.
 PR 03-APR-2000; 2000US-0194246P.
 PR 19-JUL-2000; 2000US-00619251.
 XX (CURA-) CURAGEN CORP.
 PA Shimkets RA, Vernet C, Burgess C, Fernandes E, Taupier R;
 PI Quinn KE, Spyteck KA, Rastelli L, Herrmann JL;
 XX WPI; 2001-218559/22.
 DR N-PSDB; AAF76715.
 XX Fibroblast growth factor-19X polypeptides and polynucleotides useful for
 PT diagnosis, prevention, treatment of proliferative, differentiative,
 PT tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis.
 XX Claim 11; Page 7; 97pp; English.
 CC The present invention describes the protein and coding sequences of the
 CC human fibroblast growth factor (FGF) 19 homologue FGF19X, the former of
 CC which is shown here. The sequences can be used in the prognosis and
 CC treatment of proliferative diseases such as cancer, restenosis, and
 CC psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well as
 CC to stimulate cell growth for treating neurological disorders such as
 CC Alzheimer's disease
 XX Sequence 153 AA;
 SQ
 Query Match 100.0%; Score 86; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. No. 4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQTEAH 16
 DB 45 RQRYLYTDDAQTEAH 60
 RESULT 6
 AAU00965
 ID AAU00965 standard; protein; 181 AA.
 AC AAU00965;
 XX 24-MAY-2001 (first entry)
 DT Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
 DE Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
 KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
 KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
 KW

neurodegenerative disease; haematopoietic cell reconstruction; cachexia;
 chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
 multiple sclerosis; short stature; delayed maturation; excessive growth;
 acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
 androgen target organ abnormality; respiratory distress syndrome; stroke;
 cancer; atherosclerosis; hypercholesterolemia; osteoporosis; baldness;
 osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
 decreased stamina; decreased cardiac function; immune system dysfunction;
 Parkinson's disease; Alzheimer's disease; decreased cognitive function;
 senile dementia; human.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200118172-A2.
 PD 15-MAR-2001.
 XX 05-SEP-2000; 2000WO-US024373.
 PF 07-SEP-1999; 99US-00391861.
 PR 23-AUG-2000; 2000US-00644052.
 XX (AMGE-) AMGEN INC.
 PA Thomason AR, Liu B;
 PI WPI; 2001-226743/23.
 DR Novel isolated fibroblast growth factor-like polypeptide useful for
 PT treating, preventing or ameliorating cirrhosis, inflammatory bowel
 PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
 PT osteoporosis.
 XX Claim 14; Page 116-117; 138pp; English.
 PS The sequence represents a fragment of a fibroblast growth factor-like
 CC (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid
 CC play a role in modulating body growth, maturation or life-span. They are
 CC also useful for treating, preventing or ameliorating disorders such as
 CC cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,
 CC diabetes, obesity, gastrointestinal abnormalities, neurodegenerative
 CC diseases, damage to renal tubules as a result of acute tubular necrosis,
 CC haematopoietic cell reconstruction following chemotherapy, wasting
 CC syndromes (e.g., cancer associated cachexia), damage to the corneal
 CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
 CC stature, delayed maturation, excessive growth (e.g. acromegaly),
 CC premature maturation, alopecia, abnormalities of androgen target organs,
 CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
 CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,
 CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
 CC baldness, wrinkles, increased fatigue, decreased stamina, decreased
 CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,
 CC senile dementia, Alzheimer's disease, and decreased cognitive function
 XX Sequence 181 AA;
 SQ
 Query Match 100.0%; Score 86; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQTEAH 16
 DB 17 RQRYLYTDDAQTEAH 32
 RESULT 7
 ADL57109
 ID ADL57109 standard; protein; 183 AA.
 XX ADL57109;
 AC ADL57109;
 XX 03-JUN-2004 (first entry)
 DT
 XX

DE Human NOV6a protein SEQ ID NO:54.
XX human; antidiabetic; anorectic; cardiatic; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; gene therapy;
KW fibroblast growth factor receptor 4; FGF4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX Homo sapiens.
XX WO2004022723-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-US028141.
XX 09-SEP-2002; 2002US-0409145P.
XX 10-SEP-2002; 2002US-0409544P.
XX 12-SEP-2002; 2002US-0410320P.
XX 16-SEP-2002; 2002US-0411060P.
XX 23-SEP-2002; 2002US-0412766P.
XX 23-SEP-2002; 2002US-0412825P.
XX 24-SEP-2002; 2002US-0412767P.
XX 25-SEP-2002; 2002US-0413342P.
XX 30-SEP-2002; 2002US-0414832P.
XX (CURA-) CURAGEN CORP.
XX
XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
XX WPI; 2004-315567/29.
XX N-PSDB; ADL57108.
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 54; 214pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiatic, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX

CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
XX Sequence 183 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 183;
XX Best Local Similarity 100.0%; Pred. No. 5e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
DB 17 RQRYLYTDDAQQTAAH 32
RESULT 8
AAE05078
ID AAE05078 standard; protein; 208 AA.
XX
XX AAE05078;
XX
XX 18-SEP-2001 (first entry)
XX
XX Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
XX
XX Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;
KW proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis;
KW chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture;
KW bone formation; diabetes mellitus; neural cell development; angiogenesis;
KW amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer;
KW congenital disorder; wound healing; cardiac function; glomerulonephritis;
KW surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
KW hypertension; cycostatic; vasotropic; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..27
XX Protein 28..208
XX Binding-site 44..46
XX /label= Signal_peptide
XX /label= Human_mature_zFGF11_protein
XX /note= "Heparin binding domain"
XX
XX WO200149849-A1.
XX
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US0000324.
XX
XX 05-JAN-2000; 2000US-00477886.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Conklin DC, Chen Z;
XX WPI; 2001-441880/47.
XX N-PSDB; AAD09151.
XX
XX Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast
PT growth factor family, for stimulating proliferation of mesenchymal,
PT osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
PT cancer.

```

XX PS Claim 1; Page 63; 69pp; English.
XX CC The present sequence is human fibroblast growth factor (FGF) homologue,
XX CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
XX CC for stimulating proliferation of mesenchymal cells, osteoblastic lineage
XX CC cells. zFGF11 is useful for identifying chromosomal disorders associated
XX CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
XX CC stimulation, inhibition or proliferation of myocytes, smooth muscle
XX CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
XX CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
XX CC derived cells and endothelial cells and inhibiting chondrosarcomas,
XX CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts,
XX CC results in bone formation useful for treating bone defects, fractures,
XX CC osteoporosis and other deficiencies in bone structure and formation.
XX CC zFGF11 is useful for treating disorders associated with diabetes
XX CC mellitus, neural cell development or degeneration, amyotrophic lateral
XX CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
XX CC maintenance of neuronal differentiation and congenital disorders of the
XX CC nervous system or lack of neuronal development, promoting angiogenesis
XX CC and wound healing, for revascularisation in eye, complications related to
XX CC poor circulation such as diabetic foot ulcers, improving cardiac
XX CC function, modulating surfactant production in the lung epithelium, to
XX CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
XX CC events, particularly in the heart or brain and for inducing skeletal
XX CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
XX CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
XX CC are useful for inhibiting disorders associated with kidney epithelium
XX CC such as glomerulonephritis
XX PS Sequence 208 AA;
XX CC
XX CC Query Match 100.0%; Score 86; DB 4; Length 208;
XX CC Best Local Similarity 100.0%; Pred. No. 5.7e-07;
XX CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 RQRYLYTDDAQOQTEAH 16
XX CC |||||
XX CC 44 RQRYLYTDDAQOQTEAH 59
XX CC
XX CC RESULT 9
XX CC AAU83630
XX CC ID AAU83630 standard; protein; 208 AA.
XX CC AC AAU83630;
XX CC
XX CC DT 08-MAY-2002 (first entry)
XX CC
XX CC DE Human PRO protein, Seq ID No 78.
XX CC
XX CC KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX CC breast cancer; prostate tumour; rectal tumour; liver tumour;
XX CC KW pericyte cell proliferation; chondrocyte cell proliferation;
XX CC tumour necrosis factor-alpha.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN WO200208288-A2.
XX CC PD 31-JAN-2002.
XX CC
XX CC PF 29-JUN-2001; 2001WO-US021066.
XX CC
XX CC PR 20-JUL-2000; 2000US-0219556P.
XX CC PR 25-JUL-2000; 2000US-0220585P.
XX CC PR 25-JUL-2000; 2000US-0220605P.
XX CC PR 25-JUL-2000; 2000US-0220607P.
XX CC PR 25-JUL-2000; 2000US-0220624P.
XX CC PR 25-JUL-2000; 2000US-0220638P.
XX CC PR 25-JUL-2000; 2000US-0220664P.
XX CC PR 25-JUL-2000; 2000US-0220666P.
XX CC PR 26-JUL-2000; 2000US-0220893P.
XX CC
XX PS Claim 1; Page 63; 69pp; English.
XX CC The present sequence is human fibroblast growth factor (FGF) homologue,
XX CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
XX CC for stimulating proliferation of mesenchymal cells, osteoblastic lineage
XX CC cells. zFGF11 is useful for identifying chromosomal disorders associated
XX CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
XX CC stimulation, inhibition or proliferation of myocytes, smooth muscle
XX CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
XX CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
XX CC derived cells and endothelial cells and inhibiting chondrosarcomas,
XX CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts,
XX CC results in bone formation useful for treating bone defects, fractures,
XX CC osteoporosis and other deficiencies in bone structure and formation.
XX CC zFGF11 is useful for treating disorders associated with diabetes
XX CC mellitus, neural cell development or degeneration, amyotrophic lateral
XX CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
XX CC maintenance of neuronal differentiation and congenital disorders of the
XX CC nervous system or lack of neuronal development, promoting angiogenesis
XX CC and wound healing, for revascularisation in eye, complications related to
XX CC poor circulation such as diabetic foot ulcers, improving cardiac
XX CC function, modulating surfactant production in the lung epithelium, to
XX CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
XX CC events, particularly in the heart or brain and for inducing skeletal
XX CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
XX CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
XX CC are useful for inhibiting disorders associated with kidney epithelium
XX CC such as glomerulonephritis
XX PS Sequence 208 AA;
XX CC
XX CC Query Match 100.0%; Score 86; DB 4; Length 208;
XX CC Best Local Similarity 100.0%; Pred. No. 5.7e-07;
XX CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 RQRYLYTDDAQOQTEAH 16
XX CC |||||
XX CC 44 RQRYLYTDDAQOQTEAH 59
XX CC
XX CC RESULT 9
XX CC AAU83630
XX CC ID AAU83630 standard; protein; 208 AA.
XX CC AC AAU83630;
XX CC
XX CC DT 08-MAY-2002 (first entry)
XX CC
XX CC DE Human PRO protein, Seq ID No 78.
XX CC
XX CC KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX CC breast cancer; prostate tumour; rectal tumour; liver tumour;
XX CC KW pericyte cell proliferation; chondrocyte cell proliferation;
XX CC tumour necrosis factor-alpha.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN WO200208288-A2.
XX CC PD 31-JAN-2002.
XX CC
XX CC PF 29-JUN-2001; 2001WO-US021066.
XX CC
XX CC PR 20-JUL-2000; 2000US-0219556P.
XX CC PR 25-JUL-2000; 2000US-0220585P.
XX CC PR 25-JUL-2000; 2000US-0220605P.
XX CC PR 25-JUL-2000; 2000US-0220607P.
XX CC PR 25-JUL-2000; 2000US-0220624P.
XX CC PR 25-JUL-2000; 2000US-0220638P.
XX CC PR 25-JUL-2000; 2000US-0220664P.
XX CC PR 25-JUL-2000; 2000US-0220666P.
XX CC PR 26-JUL-2000; 2000US-0220893P.
XX CC
XX PS Claim 1; Page 63; 69pp; English.
XX CC The present sequence is human fibroblast growth factor (FGF) homologue,
XX CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
XX CC for stimulating proliferation of mesenchymal cells, osteoblastic lineage
XX CC cells. zFGF11 is useful for identifying chromosomal disorders associated
XX CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
XX CC stimulation, inhibition or proliferation of myocytes, smooth muscle
XX CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
XX CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
XX CC derived cells and endothelial cells and inhibiting chondrosarcomas,
XX CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts,
XX CC results in bone formation useful for treating bone defects, fractures,
XX CC osteoporosis and other deficiencies in bone structure and formation.
XX CC zFGF11 is useful for treating disorders associated with diabetes
XX CC mellitus, neural cell development or degeneration, amyotrophic lateral
XX CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
XX CC maintenance of neuronal differentiation and congenital disorders of the
XX CC nervous system or lack of neuronal development, promoting angiogenesis
XX CC and wound healing, for revascularisation in eye, complications related to
XX CC poor circulation such as diabetic foot ulcers, improving cardiac
XX CC function, modulating surfactant production in the lung epithelium, to
XX CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
XX CC events, particularly in the heart or brain and for inducing skeletal
XX CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
XX CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
XX CC are useful for inhibiting disorders associated with kidney epithelium
XX CC such as glomerulonephritis
XX PS Sequence 208 AA;
XX CC
XX CC Query Match 100.0%; Score 86; DB 5; Length 208;
XX CC Best Local Similarity 100.0%; Pred. No. 5.7e-07;
XX CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 RQRYLYTDDAQOQTEAH 16
XX CC |||||
XX CC 44 RQRYLYTDDAQOQTEAH 59
XX CC
XX CC RESULT 10
XX CC ABG32358
XX CC ID ABG32358 standard; protein; 208 AA.
XX CC AC ABG32358;
XX CC
XX CC DT 05-NOV-2002 (first entry)
XX CC
XX CC DE Human fibroblast growth factor (FGF) homologue, zFGF11.
XX CC
XX CC KW Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR11c;
XX CC osteoblastic lineage cell; diabetes mellitus; neuropathy;
XX CC KW neural cell development; amyotrophic lateral sclerosis;

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PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 15-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX PA (GETH ) GENENTECH INC.
XX PS Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WI WPI; 2002-172001/22.
XX DR N-PSDB; ABK33574.
XX CC One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX CC useful for treating a PRO related disorder and for diagnosing tumors such
XX CC as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX CC or liver tumor.
XX PS Claim 11; Fig 78; 359pp; English.
XX CC The invention relates to one hundred and twenty two nucleic acids
XX CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX CC agonists and antagonists are useful for treating a PRO related disorder.
XX CC The PRO polypeptides are useful for diagnosing tumors, especially lung
XX CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
XX CC liver tumor. The PRO polypeptides are useful for stimulating the
XX CC proliferation of, or gene expression, in pericyte cells, for stimulating
XX CC the proliferation or differentiation of chondrocyte cells, for
XX CC stimulating the release of tumour necrosis factor-alpha from human blood,
XX CC for stimulating or inhibiting the proliferation of normal human dermal
XX CC fibroblast cells. The PRO polypeptide may also be used as molecular
XX CC weight markers and for tissue typing. The PRO nucleic acids have
XX CC applications in molecular biology, including use as hybridisation probes,
XX CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX CC protein sequences of the invention
XX PS Sequence 208 AA;
XX CC
XX CC Query Match 100.0%; Score 86; DB 5; Length 208;
XX CC Best Local Similarity 100.0%; Pred. No. 5.7e-07;
XX CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 RQRYLYTDDAQOQTEAH 16
XX CC |||||
XX CC 44 RQRYLYTDDAQOQTEAH 59
XX CC
XX CC RESULT 10
XX CC ABG32358
XX CC ID ABG32358 standard; protein; 208 AA.
XX CC AC ABG32358;
XX CC
XX CC DT 05-NOV-2002 (first entry)
XX CC
XX CC DE Human fibroblast growth factor (FGF) homologue, zFGF11.
XX CC
XX CC KW Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR11c;
XX CC osteoblastic lineage cell; diabetes mellitus; neuropathy;
XX CC KW neural cell development; amyotrophic lateral sclerosis;

```

KW cerebrovascular stroke; neuronal differentiation; congenital disorder;
 KW nervous system disorder; cardiac function; wound healing.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27 Signal sequence
 FT Protein /label= Signal sequence
 FT 28..208
 FT /note= "Mature fibroblast growth factor homologue,
 FT zFGF11. This sequence is specifically claimed in claim 4"
 XX
 XX US2002081663-A1.
 XX
 XX 27-JUN-2002.
 XX
 XX 05-JAN-2001; 2001US-00755695.
 XX
 XX 05-JAN-2000; 2000US-0174526P.
 PR
 XX (CONK/) CONKLIN D C.
 PA (CHEN/) CHEN Z.
 XX
 XX Conklin DC, Chen Z;
 XX
 XX WPI; 2002-626540/67.
 DR N-PSDB; ABK91310.
 XX
 XX Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in
 PT treatment of disorders associated with diabetes mellitus, neural cell
 PT development or degeneration, amphotrophic lateral sclerosis,
 PT cerebrovascular stroke.
 XX
 XX Claim 4; Fig 1; 35pp; English.
 PS
 XX The invention relates to an isolated human polypeptide (I) for zFGF11 (a
 CC fibroblast growth factor), and the encoding polynucleotide (II). (I) and
 CC (II) are used in methods of the invention stimulating proliferation of
 CC mesenchymal cells, detecting the presence of zFGF11 in a biological
 CC sample, detecting the presence of FGFR11c in a biological sample and
 CC stimulating proliferation of osteoblastic lineage cells. The
 CC polypeptides, nucleic acid and/or antibodies of the invention may be used
 CC in treatment of disorders associated with diabetes mellitus, neural cell
 CC development or degeneration, amphotrophic lateral sclerosis,
 CC cerebrovascular stroke, neuropathy associated with lack of maintenance of
 CC neuronal differentiation, and congenital disorders of the nervous system
 CC or lack of neuronal development. Molecules of the invention may also be
 CC useful for improving cardiac function and for promoting wound healing of
 CC the epidermis. The present sequence represents the amino acid sequence of
 CC human zFGF11
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16
 Db 44 RQRYLYTDDAQQTAAH 59
 |||||
 RESULT 11
 AAE17601
 ID AAE17601 standard; protein; 208 AA.
 XX
 AC AAE17601;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human extracellular messenger (XMES)-3 protein.
 XX
 XX Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;

KW Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
 KW acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
 KW developmental disorder; anaemia; Cushing's syndrome; endocrine disorder;
 KW vascular malformation; cell proliferative disorder; gene therapy; cancer;
 KW neuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic;
 KW hyperthyroidism; gonadal steroid hormone; pancreatic disorder; neotropic;
 KW diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
 KW antiviral; antifungal; parasitic; protozoal; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200194587-A2.
 XX
 PD 13-DEC-2001.
 XX
 XX 06-JUN-2001; 2001WO-US018476.
 PF
 XX 06-JUN-2000; 2000US-0210233P.
 PR
 XX 23-JUN-2000; 2000US-0213465P.
 PR
 XX 14-NOV-2000; 2000US-0249019P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Lal P, Yue H, He A, Nguyen DB, Walia N, Gandhi AR, Azimzai Y;
 PI Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
 PI Policky JL;
 XX
 XX WPI; 2002-154573/20.
 DR N-PSDB; AAD28493.
 XX
 XX New extracellular messenger polypeptides and polynucleotides encoding
 PT them, useful for diagnosing, treating or preventing e.g. neurological,
 PT autoimmune, inflammatory, developmental and endocrine disorders.
 XX
 XX Claim 1; Page 111; 123pp; English.
 PS
 XX The present invention relates to new extracellular messenger polypeptides
 CC and polynucleotides encoding them. XMES is useful in the diagnosis,
 CC treatment and prevention of neurological disorders (e.g. epilepsy,
 CC stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g.
 CC acquired immune deficiency syndrome, AIDS, Addison's disease, or
 CC allergies), developmental disorders (e.g. renal tubular acidosis, anaemia
 CC or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy,
 CC aneurysm or vascular malformation), and cell proliferative disorders
 CC (e.g. cancer), and in the assessment of the effects of exogenous
 CC compounds on the expression of nucleic acid and amino acid sequences of
 CC extracellular messengers. XMES may also be used in the treatment of
 CC viral, bacterial, fungal, parasitic, protozoal and helminthic
 CC infections, trauma, disorders associated with hypopituitarism,
 CC hypothyroidism, hyperthyroidism or gonadal steroid hormones, and
 CC pancreatic disorders such as type I or type II diabetes mellitus. The
 CC XMES may be used for somatic or germline gene therapy. The present
 CC sequence is human XMES-3 protein
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16
 Db 44 RQRYLYTDDAQQTAAH 59
 |||||
 RESULT 12
 ABUS0777
 ID ABUS0777 standard; protein; 208 AA.
 XX
 AC ABUS0777;
 XX
 DT 23-JUN-2003 (first entry)
 XX

DE Human PRO polypeptide #39.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US031086.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-342045/32.
DR N-PSDB; ACA66879.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides;
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. AB080739-AB080860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/paipsDIDentry.html
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 44 RQRYLYTDDAQOQTEAH 59

RESULT 13
AB033743
ID AB033743 standard; protein; 208 AA.
XX
XX AB033743;
AC
XX 17-SEP-2003 (first entry)
DT
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; biosector; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX

OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR N-PSDB; ACD68631.
XX
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioeffectors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 44 RQRYLYTDDAQOQTEAH 59

RESULT 14
ABU82086
ID ABU82086 standard; protein; 208 AA.
XX
XX ABU82086;
AC
XX 25-JUN-2003 (first entry)
DT
XX
DE Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX US200308063-A1.
XX
PD 08-MAY-2003.
XX
PF 12-AUG-2002; 2002US-00219003.
XX
PR 25-JUL-2000; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-393229/37.
DR N-PSDB; ACA68335.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
CC The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 208 AA;
Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 15
ABP96156
ID ABP96156 standard; protein; 208 AA.
XX
AC ABP96156;
XX
DT 12-MAY-2003 (first entry)
XX
DE Human fibroblast growth factor 21 protein SEQ ID NO:2.
XX
KW Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter;
KW diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;

type 1 diabetes.
XX
OS Homo sapiens.
XX WO2003011213-A2.
XX
PD 13-FEB-2003.
XX
PF 22-JUL-2002; 2002WO-US021290.
XX
PR 30-JUL-2001; 2001US-0308702P.
PR 10-JAN-2002; 2002US-0347991P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Glasebrook AL, Hammond LJ, Kharitonkov A, Shiyanova TL;
XX WPI: 2003-248106/24.
DR N-PSDB; ABZ79797.
XX
PT Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or
PT obesity, by administering composition comprising fibroblast growth factor
PT -21.
XX
PS Claim 3; Fig 1; 32pp; English.
XX
CC The present sequence represents human fibroblast growth factor 21 (FGF-
CC 21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
CC qter. The present invention describes a method for treating a mammal
CC exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for
CC obesity which comprises administering to the mammal a composition
CC comprising FGF-21 which has at least 95% amino acid sequence identity to
CC the 208 amino acid sequence given in ABP96156. Also described: (1)
CC inducing an increase in glucose uptake in adipocyte cells by
CC administering FGF-21 to induce an increase in glucose uptake; and (2)
CC manufacturing a medicament for treating type 1 diabetes; type 2 diabetes
CC or obesity in a mammal using FGF-21 having 95% amino acid sequence
CC identity to ABP96156. FGF-21 has antidiabetic and anorectic activities.
CC The method is useful for treating a mammal exhibiting type 2 or 1
CC diabetes or for treating a mammal for obesity. The method is preferably
CC useful for treating humans exhibiting type 1 or type 2 diabetes, and for
CC treating domestic animals for obesity
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59

Search completed: July 8, 2005, 22:13:08
Job time : 21.9333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:04:53 ; Search time 5.4 Seconds
(without alignments)
221.182 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQOQTEAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	4	US-09-715-805-7
2	86	100.0	85	4	US-09-621-976-5213
3	86	100.0	181	4	US-09-390-207-5
4	86	100.0	209	4	US-09-390-207-2
5	86	100.0	209	4	US-09-715-805-4
6	75	87.2	181	4	US-09-390-207-6
7	75	87.2	210	4	US-09-390-207-4
8	75	87.2	210	4	US-09-715-805-2
9	48	55.8	479	4	US-09-489-039A-14225
10	42	48.8	137	4	US-09-107-532A-4355
11	41	47.7	1121	3	US-09-171-461-28
12	41	47.7	1121	4	US-09-970-711-28
13	40	46.5	102	4	US-09-248-796A-26424
14	40	46.5	152	4	US-09-252-991A-28391
15	40	46.5	366	4	US-09-489-039A-10181
16	40	46.5	566	4	US-09-538-092-581
17	39	45.3	735	3	US-09-147-236-7
18	39	45.3	735	4	US-09-523-474-7
19	38	44.2	83	4	US-09-513-999C-4553
20	38	44.2	83	4	US-09-471-276-1470
21	38	44.2	136	4	US-09-621-976-4224
22	38	44.2	164	4	US-09-634-238-396
23	38	44.2	285	4	US-09-489-039A-14221
24	38	44.2	301	4	US-09-710-279-1396
25	38	44.2	526	4	US-09-489-039A-10731
26	38	44.2	557	3	US-09-134-001C-5569
27	38	44.2	580	4	US-09-830-433A-20

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28 38 44.2 747 3 US-08-089-397A-16 Sequence 16, Appl
29 38 44.2 776 1 US-07-603-133B-17 Sequence 17, Appl
30 38 44.2 776 1 US-07-603-133B-20 Sequence 20, Appl
31 38 44.2 776 3 US-08-089-397A-15 Sequence 15, Appl
32 38 44.2 2396 1 US-08-157-005-2 Sequence 2, Appl
33 38 44.2 2396 3 US-08-747-863-2 Sequence 2, Appl
34 38 44.2 2396 4 US-09-565-864-2 Sequence 2, Appl
35 38 44.2 2396 4 US-10-226-065-2 Sequence 2, Appl
36 37 43.0 219 4 US-09-710-279-2206 Sequence 2206, Ap
37 37 43.0 310 4 US-09-252-991A-31483 Sequence 31483, A
38 37 43.0 317 3 US-09-134-001C-3993 Sequence 3993, Ap
39 37 43.0 318 4 US-09-540-236-2086 Sequence 2086, Ap
40 37 43.0 338 4 US-09-543-681A-5499 Sequence 5499, Ap
41 37 43.0 349 4 US-09-270-767-42579 Sequence 42579, A
42 37 43.0 377 3 US-09-352-990-28 Sequence 28, Appl
43 37 43.0 400 4 US-09-252-991A-29728 Sequence 29728, A
44 37 43.0 415 4 US-09-538-092-320 Sequence 320, App
45 37 43.0 497 4 US-09-543-681A-6926 Sequence 6926, Ap

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ALIGNMENTS

RESULT 1

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US-09-715-805-7
; Sequence 7, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanagh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715,805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-7

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Query Match 100.0%; Score 86; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.le-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RQRYLYTDDAQOQTEAH 16
Db 1 RQRYLYTDDAQOQTEAH 16

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RESULT 2

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US-09-621-976-5213
; Sequence 5213, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SIGNAL
; NAME/KEY: -28...-1

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; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-5213

Query Match      100.0%; Score 86; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      45 RORYLYTDDAQOQTEAH 60

RESULT 3
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match      100.0%; Score 86; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      17 RORYLYTDDAQOQTEAH 32

RESULT 4
US-09-390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match      100.0%; Score 86; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      45 RORYLYTDDAQOQTEAH 60

; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-5213

Query Match      100.0%; Score 86; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      45 RORYLYTDDAQOQTEAH 60

RESULT 5
US-09-715-805-4
; Sequence 4, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715,805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-4

Query Match      100.0%; Score 86; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      45 RORYLYTDDAQOQTEAH 60

RESULT 6
US-09-390-207-6
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6

Query Match      87.2%; Score 75; DB 4; Length 181;
Best Local Similarity 87.5%; Pred. No. 3.1e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RORYLYTDDAQOQTEAH 16
Db      17 RORYLYTDDAQOQTEAH 32

RESULT 7
US-09-390-207-4
; Sequence 4, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 210
; TYPE: PRT
US-09-390-207-4
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; ORGANISM: Mus musculus
US-09-390-207-4
Query Match      87.2%; Score 75; DB 4; Length 210;
Best Local Similarity 87.5%; Pred. No. 3.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 46 RQRYLYTDDQOQTEAH 61

RESULT 8
US-09-715-805-2
; Sequence 2, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715,805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-715-805-2
Query Match      87.2%; Score 75; DB 4; Length 210;
Best Local Similarity 87.5%; Pred. No. 3.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 46 RQRYLYTDDQOQTEAH 61

RESULT 9
US-09-489-039A-14225
; Sequence 14225, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14225
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14225
Query Match      55.8%; Score 48; DB 4; Length 479;
Best Local Similarity 62.5%; Pred. No. 3.5;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 460 RQRYHPGDDRQOQPAH 475

RESULT 10
US-09-107-532A-4355
; Sequence 4355, Application US/09107532A
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; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...137
; SEQUENCE DESCRIPTION: SEQ ID NO: 4355:
US-09-107-532A-4355
Query Match      48.8%; Score 42; DB 4; Length 137;
Best Local Similarity 54.5%; Pred. No. 9.6;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YLYTDDAQQTE 14
   |||||
Db 108 YLYTDESDETE 118

RESULT 11
US-09-171-461-28
; Sequence 28, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chiocca, Susanna
; APPLICANT: Kurzbauer, Robert
; APPLICANT: Schaifner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; EARLIER FILING DATE: 1997-04-18
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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1121
; TYPE: PRT
; ORGANISM: CELO VIRUS
; FEATURE:
; OTHER INFORMATION: Position: 6501...9866/Product: E2b pol
US-09-171-461-28

Query Match          47.7%; Score 41; DB 3; Length 1121;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTE 14
Db 731 RQFRYADDPQEE 744

RESULT 12
US-09-970-711-28
; Sequence 28, Application US/09970711
; Patent No. 6773709
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chiocca, Susanna
; APPLICANT: Kurzbaue, Robert
; APPLICANT: Schaffner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800001
; CURRENT APPLICATION NUMBER: US/09/970,711
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/171,461
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: PCT/EP97/01944
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1121
; TYPE: PRT
; ORGANISM: CELO VIRUS
; FEATURE:
; OTHER INFORMATION: Position: 6501...9866/Product: E2b pol
US-09-970-711-28

Query Match          47.7%; Score 41; DB 4; Length 1121;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTE 14
Db 731 RQFRYADDPQEE 744

RESULT 13
US-09-248-796A-26424
; Sequence 26424, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26424
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; LENGTH: 102
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26424

Query Match          46.5%; Score 40; DB 4; Length 102;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTEAH 16
Db 75 KQVYTFWDDVQEIQSH 90

RESULT 14
US-09-252-991A-28391
; Sequence 28391, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28391
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28391

Query Match          46.5%; Score 40; DB 4; Length 152;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 YTDDAQOTEAH 16
Db 129 WRDDAPQTESH 139

RESULT 15
US-09-489-039A-10181
; Sequence 10181, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10181
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10181

Query Match          46.5%; Score 40; DB 4; Length 366;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RYLTYDDAQOTEAH 16
Db 83 RYIYTDNQKKNWH 96
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Search completed: July 8, 2005, 22:22:33
Job time : 6.4 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:18:21 ; Search time 19.0667 Seconds
(without alignments)
324.193 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQOTEAH 16

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Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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SUMMARIES

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1	86	100.0	16	13 US-10-060-765-7	Sequence 7, Appli
2	86	100.0	16	16 US-10-818-140-7	Sequence 7, Appli
3	86	100.0	16	17 US-10-771-173-7	Sequence 7, Appli
4	86	100.0	91	17 US-10-659-004-60	Sequence 60, Appl
5	86	100.0	125	17 US-10-659-004-52	Sequence 52, Appl
6	86	100.0	136	9 US-09-901-938-33	Sequence 33, Appl
7	86	100.0	136	14 US-10-379-334-33	Sequence 33, Appl
8	86	100.0	183	17 US-10-659-004-54	Sequence 54, Appl
9	86	100.0	208	9 US-09-755-695-2	Sequence 2, Appli
10	86	100.0	208	14 US-10-227-884-78	Sequence 78, Appl
11	86	100.0	208	14 US-10-230-163-78	Sequence 78, Appl

12	86	100.0	208	14	US-10-230-338-78	Sequence 78, Appl
13	86	100.0	208	14	US-10-218-631-78	Sequence 78, Appl
14	86	100.0	208	14	US-10-230-414-78	Sequence 78, Appl
15	86	100.0	208	14	US-10-232-224-78	Sequence 78, Appl
16	86	100.0	208	14	US-10-216-159A-78	Sequence 78, Appl
17	86	100.0	208	14	US-10-218-849-78	Sequence 78, Appl
18	86	100.0	208	14	US-10-227-873-78	Sequence 78, Appl
19	86	100.0	208	14	US-10-227-883-78	Sequence 78, Appl
20	86	100.0	208	14	US-10-219-076-78	Sequence 78, Appl
21	86	100.0	208	14	US-10-230-434-78	Sequence 78, Appl
22	86	100.0	208	14	US-10-219-003-78	Sequence 78, Appl
23	86	100.0	208	14	US-10-219-075-78	Sequence 78, Appl
24	86	100.0	208	14	US-10-219-464-78	Sequence 78, Appl
25	86	100.0	208	14	US-10-219-466-78	Sequence 78, Appl
26	86	100.0	208	14	US-10-219-479-78	Sequence 78, Appl
27	86	100.0	208	14	US-10-219-481-78	Sequence 78, Appl
28	86	100.0	208	14	US-10-230-260-78	Sequence 78, Appl
29	86	100.0	208	14	US-10-232-231-78	Sequence 78, Appl
30	86	100.0	208	14	US-10-232-233-78	Sequence 78, Appl
31	86	100.0	208	14	US-10-216-165-78	Sequence 78, Appl
32	86	100.0	208	14	US-10-218-956-78	Sequence 78, Appl
33	86	100.0	208	14	US-10-219-468-78	Sequence 78, Appl
34	86	100.0	208	14	US-10-219-478-78	Sequence 78, Appl
35	86	100.0	208	14	US-10-219-536-78	Sequence 78, Appl
36	86	100.0	208	14	US-10-233-205-78	Sequence 78, Appl
37	86	100.0	208	14	US-10-219-072-78	Sequence 78, Appl
38	86	100.0	208	14	US-10-219-470-78	Sequence 78, Appl
39	86	100.0	208	14	US-10-219-474-78	Sequence 78, Appl
40	86	100.0	208	14	US-10-219-524-78	Sequence 78, Appl
41	86	100.0	208	14	US-10-219-528-78	Sequence 78, Appl
42	86	100.0	208	14	US-10-227-880-78	Sequence 78, Appl
43	86	100.0	208	14	US-10-227-881-78	Sequence 78, Appl
44	86	100.0	208	14	US-10-227-882-78	Sequence 78, Appl
45	86	100.0	208	14	US-10-230-436-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-10-060-765-7
; Sequence 7, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060.765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-7

Query Match 100.0%; Score 86; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTEAH 16

Db 1 RQRYLYTDDAQOTEAH 16

RESULT 2

US-10-818-140-7

; Sequence 7, Application US/10818140


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Query Match      100.0%; Score 86; DB 17; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 17 RQRYLYTDDAQOQTEAH 32

RESULT 6
US-09-901-938-33
; Sequence 33, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-901-938-33

Query Match      100.0%; Score 86; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 7 RQRYLYTDDAQOQTEAH 22

RESULT 7
US-10-379-334-33
; Sequence 33, Application US/10379334
; Publication No. US20030181379A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/10/379,334
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/901,938
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-379-334-33

Query Match      100.0%; Score 86; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 7 RQRYLYTDDAQOQTEAH 22
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RESULT 8
US-10-659-004-54
; Sequence 54, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
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; PRIOR FILING DATE: 2001-06-14
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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
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; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-004-54
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Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RQRYLYTDDAQOQTEAH 16
DB 17 RQRYLYTDDAQOQTEAH 32

RESULT 9
US-09-755-695-2
; Sequence 2, Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; FILE REFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09/755,695
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/174,526
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2
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Best Local Similarity 100.0%; Pred. No. 1.7e-06;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16
DB 44 RQRYLYTDDAQQTAAH 59

RESULT 10
US-10-227-884-78
; Sequence 78, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
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; PRIOR APPLICATION NUMBER: 60/095916
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; PRIOR FILING DATE: 1998-11-17
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; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
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;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
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;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
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;; PRIOR FILING DATE: 1999-04-26
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;; PRIOR FILING DATE: 1999-06-22
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;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
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;; PRIOR APPLICATION NUMBER: 60/149320
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;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.08; Score 86; DB 14; Length 208;

Best Local Similarity 100.08; Pred. No. 1.7e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;
Qy 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59

RESULT 11
US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
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; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
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; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/101922
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; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
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; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565

; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
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; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 12

US-10-230-338-78
; Sequence 78, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C92
CURRENT APPLICATION NUMBER: US/10/230,338
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
TYPE: PRT
ORGANISM: Homo Sapien
US-10-230-338-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTEAH 16
DB 44 RQRYLYTDDAQQTEAH 59

RESULT 13
US-10-218-631-78
Sequence 78, Application US/10218631
Publication No. US20030045687A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C14
CURRENT APPLICATION NUMBER: US/10/218,631
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
TYPE: PRT
ORGANISM: Homo Sapien
US-10-218-631-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTEAH 16
DB 44 RQRYLYTDDAQQTEAH 59

RESULT 14
US-10-230-414-78
Sequence 78, Application US/10230414
Publication No. US2003005048A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C98
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25

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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred.No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQRYLYTDDAQOQTEAH 16
Db      44 RQRYLYTDDAQOQTEAH 59

Search completed: July 8, 2005, 22:44:50
Job time : 20.0667 secs

RESULT 15
US-10-232-224-78
; Sequence 78, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred.No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RQRYLYTDDAQOQTEAH 16
Db      44 RQRYLYTDDAQOQTEAH 59

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Search completed: July 8, 2005, 22:44:50
Job time : 20.0667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:03:50 ; Search time 3.93333 Seconds
(without alignments)
391.390 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQOQTEAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	53.5	349	T00526	probable GDSL-moti
2	43	50.0	2225	T26063	hypothetical prote
3	41	47.7	93	S28726	hypothetical prote
4	41	47.7	349	T00525	probable GDSL-moti
5	40	46.5	332	T25023	hypothetical prote
6	40	46.5	403	C70385	hypothetical prote
7	40	46.5	529	JF0181	oligo-1,6-glucosid
8	40	46.5	543	B34612	zinc finger protei
9	40	46.5	566	S59382	hypothetical prote
10	40	46.5	776	VFXRYM	outer layer protei
11	40	46.5	1661	T21986	hypothetical prote
12	40	46.5	1663	T21993	hypothetical prote
13	39	45.3	259	C36819	C11 protein - rabb
14	39	45.3	263	G90294	hypothetical prote
15	39	45.3	278	T18857	hypothetical prote
16	39	45.3	439	B95927	probable sugar upt
17	39	45.3	627	T11663	probable phosphor
18	39	45.3	735	JC5869	beta-glucosidase (
19	38	44.2	235	T33962	hypothetical prote
20	38	44.2	285	A10633	probable membrane
21	38	44.2	344	T01629	probable GDSL-moti
22	38	44.2	457	B64790	yciB protein - Esc
23	38	44.2	460	T28555	probable resistanc
24	38	44.2	460	B90705	probable resistanc
25	38	44.2	580	F81042	hemolysin activati
26	38	44.2	580	A81989	probable periplasm
27	38	44.2	747	VFXR4S	outer layer protei
28	38	44.2	775	JQ1638	outer layer protei
29	38	44.2	775	JQ1639	outer layer protei

30	38	44.2	775	1	VFXRT2	outer layer protei
31	38	44.2	776	1	JQ2022	outer layer protei
32	38	44.2	776	1	VFXRB3	outer layer protei
33	38	44.2	776	1	VFXRS1	outer layer protei
34	38	44.2	776	1	VFXRT1	outer layer protei
35	38	44.2	776	2	S24410	hypothetical outer
36	38	44.2	776	2	S03611	outer layer protei
37	38	44.2	792	2	B82756	organic solvent to
38	38	44.2	1051	2	T48933	WD repeat domain p
39	38	44.2	1308	2	B32494	transposable eleme
40	38	44.2	1426	2	A99580	hypothetical prote
41	38	44.2	1619	2	T18499	hypothetical prote
42	38	44.2	1645	2	AG1897	two-component hydr
43	38	44.2	2396	2	B36861	orf 1a protein - L
44	37	43.0	101	2	D55545	afaa protein - Esc
45	37	43.0	145	2	AE3288	hypothetical prote

ALIGNMENTS

RESULT 1

T00526

probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T20K24.7

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00526; A84572

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, July 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.

A:Reference number: Z14167

A:Accession: T00526

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-349 <ROU>

A:Cross-references: UNIPROT:O64469; EMBL:AC002392; NID:g3176701; PID:g3176708

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <STO>

A:Cross-references: GB:AE002093; NID:g3176708; PIDN:AAD12024.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g19060; T20K24.7

A:Map position: 2

A:Introns: 81/1; 122/3; 197/3; 282/1

C:Superfamily: myrosinase-associated protein MyAP

Query Match 53.5%; Score 46; DB 2; Length 349;
Best Local Similarity 53.3%; Pred. No. 2.2;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 2

T26063

hypothetical protein W01F3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26063

R:Cummings, P.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20145

A;Accession: T26063
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: UNIPROT:O45881; EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3
A;Experimental source: clone W01F3
C;Genetics:
A;Gene: CESP:W01F3.3
A;Map position: 5
A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
Query Match 50.0%; Score 43; DB 2; Length 2225;
Best Local Similarity 53.8%; Pred. No. 63;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 QRYLYTDDAQQT 14
|||:|:|:|
Db 477 QRYFYNEDSQKE 489
|||:|:|:|
RESULT 3
S28726
hypothetical protein 1 (insertion sequence ISL1) - Lactobacillus casei
C;Species: Lactobacillus casei
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S28726
R;Shimizu-Kadota, M.; Kiwaki, M.; Hirokawa, H.; Tsuchida, N.
Mol. Gen. Genet. 200, 193-198, 1985
A;Title: ISL1: a new transposable element in Lactobacillus casei.
A;Reference number: S28726; MUID:85295506; PMID:2993817
A;Accession: S28726
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-93 <SHI>
A;Cross-references: UNIPROT:P71428; EMBL:X02734; NID:g1279518; PIDN:CAA26516.1; PID:g439
A;Experimental source: insertion sequence ISL1; strain C239
C;Genetics:
A;Mobile element: insertion sequence ISL1
A;Superfamily: Shigella flexneri conserved hypothetical protein tnpJ
Query Match 47.7%; Score 41; DB 2; Length 93;
Best Local Similarity 61.5%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RORYLYTDDAQQT 13
|||:|:|:|
Db 43 RWRKLYTDEGKQT 55
|||:|:|:|
RESULT 4
T00525
probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T20K24.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00525; H84571
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A;Reference number: Z14167
A;Accession: T00525
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-349 <ROU>
A;Cross-references: UNIPROT:O64468; EMBL:AC002392; NID:g3176701; PID:g3176707
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.V.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, J. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: H84420; MUID:20083487; PMID:10617197
A;Accession: H84571

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <STO>
A;Cross-references: GB:AE002093; NID:g3176707; PIDN:AAD12023.1; GSPDB:GN00139
C;Genetics:
A;Gene: T20K24.6; At2g19050
A;Map position: 2
A;Introns: 82/1; 123/3; 198/3; 281/1
C;Superfamily: myrosinase-associated protein MyAP
Query Match 47.7%; Score 41; DB 2; Length 349;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 RORYLYTDDAQQT 15
|||:|:|:|
Db 309 QRRYVYWDNVHSTEA 323
|||:|:|:|
RESULT 5
T25023
hypothetical protein T20B3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25023
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19970
A;Accession: T25023
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-332 <WIL>
A;Cross-references: UNIPROT:Q9XUN3; EMBL:Z81593; PIDN:CAB04743.1; GSPDB:GN00023; CESP:T2
A;Experimental source: clone T20B3
C;Genetics:
A;Gene: CESP:T20B3.5
A;Map position: 5
A;Introns: 110/1; 246/3
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2
Query Match 46.5%; Score 40; DB 2; Length 332;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RORYLYTDDAQQT 16
|||:|:|:|
Db 8 RTDYIHTADFOQTVLH 23
|||:|:|:|
RESULT 6
C70385
hypothetical protein aq_985 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: C70385
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov; V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Cross-references: UNIPROT:O67110; GB:AB000717; NID:g2983492; PIDN:AAC07076.1; PID:g298
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: C70385
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-403 <AP>
A;Cross-references: UNIPROT:O67110; GB:AB000717; NID:g2983492; PIDN:AAC07076.1; PID:g298
A;Experimental source: strain VP5
C;Genetics:
A;Gene: aq_985
Query Match 46.5%; Score 40; DB 2; Length 403;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
DB 85 QKRYVYVTRSEDETH 100

RESULT 7

JE0181

Oligo-1,6-glucosidase (EC 3.2.1.10) - Bacillus flavocaldarius KP1228

C:Species: Bacillus flavocaldarius KP1228

C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

C:Accession: JE0181

R:Kaewiwabara, S.; Matsuki, Y.; Kishimoto, T.; Suzuki, Y.

Biosci. Biotechnol. Biochem. 62, 1093-1102, 1998

A:Title: Clustered proline residues around the active-site cleft in thermostable oligo-1

A:Reference number: JE0181; MUID:98357218; PMID:9692189

A:Accession: JE0181

A:Molecule type: DNA

A:Residues: 1-529 <KAS>

A:Cross-references: UNIPROT:Q9P237; DDBJ:AB003697

C:Superfamily: alpha-glucosidase; alpha-amylase core homology

C:Keywords: glycosidase; hydrolase

Query Match 46.5%; Score 40; DB 2; Length 529;
Best Local Similarity 43.8%; Pred. No. 42;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
DB 227 RHELYTDEQPTAY 242

RESULT 8

B34612

zinc finger protein ZNF8 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

C:Accession: B34612

R:Lania, L.; Dotti, E.; Panmuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia

Genomics 6, 333-340, 1990

A:Title: cDNA isolation, expression analysis, and chromosomal localization of two human

A:Reference number: A34612; MUID:90169993; PMID:2106481

A:Accession: B34612

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-543 <LAN>

A:Cross-references: UNIPROT:P17098; GB:M29581; NID:G340447; PIDN:AAAG1314.1; PID:G340448

C:Genetics:

A:Gene: GDB:ZNF8

A:Cross-references: GDB:120510; OMIM:194532

A:Map position: 20q13-20q13

C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

C:Keywords: DNA binding; zinc finger

Query Match 46.5%; Score 40; DB 2; Length 543;
Best Local Similarity 53.3%; Pred. No. 43;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTE 15
DB 164 RGEYLYTDSQITDS 178

RESULT 9

S59382

hypothetical protein YLR417w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9931.3

C:Species: Saccharomyces cerevisiae

C:Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: S59382

R:Favella, A.

submitted to the EMBL Data Library, January 1995

A:Description: The sequence of S. cerevisiae cosmid 9931.

A:Reference number: S59376

A:Accession: S59382

A:Molecule type: DNA

A:Residues: 1-566 <FAV>

A:Cross-references: UNIPROT:Q06696; EMBL:U20162; NID:G632669; PIDN:AB67493.1; PID:G6326

A:Experimental source: strain S288C (AB972)

C:Genetics:

A:Gene: SGD:VPS36

A:Cross-references: SGD:S0004409; MIPS:YLR417w

A:Map position: 12R

Query Match

Best Local Similarity 46.5%; Score 40; DB 2; Length 566;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
DB 52 QRIIVIDDAKPTQ 64

RESULT 10

VPXRYM

outer layer protein VP3 - porcine rotavirus C (strain YM)

N:Alternate names: hemagglutinin; VP4 protein

N:Contains: outer layer protein VP5; outer layer protein VP8

C:Species: porcine rotavirus C

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: A40342

R:Lopez, S.; Lopez, I.; Romero, P.; Mendez, E.; Soberon, X.; Arias, C.F.

J. Virol. 65, 3738-3745, 1991

A:Title: Rotavirus YM gene 4: analysis of its deduced amino acid sequence and prediction

A:Reference number: A40342; MUID:91251227; PMID:1645789

A:Accession: A40342

A:Molecule type: genomic RNA

A:Residues: 1-776 <LOP>

A:Cross-references: UNIPROT:P25174; GB:M63231; NID:G333323; PIDN:AAA47100.1; PID:G333324

C:Superfamily: rotavirus outer layer protein VP3

C:Keywords: capsid protein; coat protein; glycoprotein; hemagglutinin

F:1-241/Product: outer layer protein VP8 #status predicted <VP8>

F:1242-247/Region: cleavage processing #status predicted

F:248-776/Product: outer layer protein VP5 #status predicted <VP5>

F:17,32,56,97,116,132,151,178,183,198,325,670/Binding site: carbohydrate (Asn) (covalent

Query Match 46.5%; Score 40; DB 1; Length 776;

Best Local Similarity 50.0%; Pred. No. 65;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOTEAH 16
DB 302 QYTYRDEGQITAH 315

RESULT 11

T21986

hypothetical protein F39B2.4a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21986

R:Dobson, R.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19498

A:Accession: T21986

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1661 <WIL>

A:Cross-references: EMBL:Z92834; PIDN:CAB07385.1; GSPDB:GN00019; CESP:F39B2.4a

A:Experimental source: clone F39B2

C:Genetics:

A:Gene: CESP:F39B2.4a

A:Map position: 1

A:Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941/3; 9

Query Match

Best Local Similarity 46.5%; Score 40; DB 2; Length 1661;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:54:48 ; Search time 19.2667 Seconds
(without alignments)
425.256 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRVLYTDDAQQTAAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	209	1 FGFL_HUMAN	Q9nsal homo sapien
2	86	100.0	209	2 Q8N683	Q8n683 homo sapien
3	75	87.2	208	2 Q8V180	Q8v180 rattus norv
4	75	87.2	210	1 FGFL_MOUSE	Q9jini mus musculu
5	46	53.5	349	2 Q64459	Q64459 arabidopsis
6	44	51.2	567	2 Q758A5	Q758a5 ashbya gos
7	43	50.0	233	2 Q65610	Q65610 kairi virus
8	43	50.0	622	2 Q6BPY1	Q6bpy1 debaryomyce
9	43	50.0	1916	2 Q8IBC1	Q8ibc1 plasmodium
10	43	50.0	2225	2 Q45881	Q45881 caenorhabdi
11	41.5	48.3	660	2 Q63KM0	Q63km0 burkholderi
12	41.5	48.3	671	2 Q62CG0	Q62cg0 burkholderi
13	41	47.7	93	2 P71428	P71428 lactobacill
14	41	47.7	243	2 Q7XAQ1	Q7xaq1 houttuynia
15	41	47.7	349	2 Q64468	Q64468 arabidopsis
16	41	47.7	355	2 Q7XMQ2	Q7xm2 oryza sativ
17	41	47.7	355	2 Q9FSS1	Q9fsa1 oryza sativ
18	41	47.7	385	2 Q48525	Q48525 lactobacill
19	41	47.7	415	1 HEMI_NEIGO	Q9zhd6 neisseria g
20	41	47.7	712	2 Q64XE9	Q64xe9 bacteroides
21	41	47.7	1031	2 Q8GSK2	Q8gsk2 bifidobacte
22	41	47.7	1121	1 DPOL_ADEG1	Q64751 avian adeno
23	41	47.7	1255	2 Q6TGL5	Q6tgl5 avian adeno
24	41	47.7	1255	2 Q7M5G2	Q7m5g2 avian adeno
25	40.5	47.1	712	2 Q6PDG4	Q6pdg4 acinetobact
26	40	46.5	174	2 Q6SYX7	Q6syx7 klebsiella
27	40	46.5	203	2 Q6CT95	Q6ct95 kluyveromyce
28	40	46.5	323	2 Q6BKQ9	Q6bkq9 debaryomyce
29	40	46.5	332	2 Q9XUN3	Q9xun3 caenorhabdi
30	40	46.5	401	2 Q6A570	Q6a570 bradyrhizob
31	40	46.5	403	2 Q6U5L8	Q6u5l8 nautilia mac

32 40 46.5 403 2 Q67110 aquifex aeo
33 40 46.5 466 1 CMT1_CRYNE
34 40 46.5 506 2 Q8L341
35 40 46.5 518 2 Q8T0C8
36 40 46.5 529 2 Q9F237 bacillus fl
37 40 46.5 529 2 Q9RA62
38 40 46.5 537 2 Q708G0
39 40 46.5 543 1 ZN08_HUMAN
40 40 46.5 566 2 Q06696
41 40 46.5 567 2 Q07SD2
42 40 46.5 575 2 Q6P199
43 40 46.5 775 2 P89057
44 40 46.5 776 1 VP24_ROTTPY
45 40 46.5 819 2 Q6PCZ6

ALIGNMENTS

RESULT 1
ID FGFL_HUMAN STANDARD; PRT; 209 AA.
AC Q9NSA1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).
GN Name=FGF21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE OF 29-43.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; AB021975; BAA99415.1; -.
DR EMBL; AY359086; AAQ89444.1; -.
DR HSSP; P03968; 1BAR.
DR Genew; HGNC:3678; FGF21.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PROSITE; PS00247; HBGF_FGF; FALSE NEG.
DR Direct protein sequencing; Growth factor; Signal.
FT SIGNAL 1 28 Fibroblast growth factor-21.
FT CHAIN 29 209 Missing (in Ref. 2).
FT CONFLICT 23 23 Missing (in Ref. 2).
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 86; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 45 RQRYLYTDDAQOQTEAH 60

RESULT 2
Q8N683 PRELIMINARY; PRT; 209 AA.
AC Q8N683;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
GN Name=FGF21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
EMBL; BC018404; AAH18404.1; -.
DR HSSP; O95750; 1PWA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PROSITE; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
KW Growth factor.
SQ SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 45 RQRYLYTDDAQOQTEAH 60

RESULT 3
Q8VI80 PRELIMINARY; PRT; 208 AA.
AC Q8VI80;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
GN Name=FGF21;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RA Itoh N.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
EMBL; AB078901; BAB84299.1; -.
DR EMBL; O95750; 1PWA.
DR HSSP; O95750; 1PWA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PROSITE; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
KW Growth factor.
SQ SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;

Query Match 87.2%; Score 75; DB 2; Length 208;
Best Local Similarity 87.5%; Pred. No. 3.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 46 RQRYLYTDDAQOQTEAH 61

RESULT 4
FGFL_MOUSE
ID FGFL_MOUSE STANDARD; PRT; 210 AA.
AC Q9JUN1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21).
GN Name=fgf21;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
RT the liver";
RL Biochim. Biophys. Acta 1492:203-206 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Otsu R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gofjohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matusda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kana A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagava A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J.C., Ring B.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Iehii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also
CC expressed in the thymus at lower levels.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
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CC -----
DR EMBL; AB025718; BAA99416.1; -;
DR EMBL; AK007574; BAB25115.1; -;
DR EMBL; EC049592; AAH49592.1; -;
DR HSSP; P08620; 11JT.
DR MGD; MGI:1861377; Fgf21.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F_Growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00263; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 210 Fibroblast growth factor-21.
SQ SEQUENCE 210 AA; 23237 MW; AS02AABA6477E6F0 CRC64;
Query Match 87.2%; Score 75; DB 1; Length 210;
Best Local Similarity 87.5%; Pred. No. 3.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RQRYLYTDDAQOQTEAH 16
Db 46 RQRYLYTDDQOQTEAH 61
RESULT 5
OC64469 PRELIMINARY; PRT; 349 AA.
AC 064469;
DC 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative GDSL-motif lipase/hydrolase.
GN Name=Ac2g19060;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Sonerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002392; AADI2024.1; -;
DR PIR; T00526; T00526.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hydrolase.
SQ SEQUENCE 349 AA; 38724 MW; 8836B8DF2AAE2AF7 CRC64;
Query Match 53.5%; Score 46; DB 2; Length 349;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RQRYLYTDDAQOQTEA 15
Db 310 RERYVYDWNVHSTEA 324

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RESULT 6
Q758A5
ID Q758A5 PRELIMINARY; PRT; 567 AA.
AC Q758A5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ABL153Wp.
GN ORFNames=ABL153W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Gates K., Dietrich F.S., Brachet S., Voegeli S.E., Lerch A.,
RA Philippsen P., Gaffney T., to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 WD repeats.
DR EMBL; AB016818; AAS2533.1; -.
DR AGD; ABL153W; -.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
SQ SEQUENCE 567 AA; 62678 MW; 51BE672E94A0309B CRC64;

Query Match 51.2%; Score 44; DB 2; Length 567;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
|:|:|:|:|:|:|:|:|:|
DB 299 RRRYHVTWDLMTTAAH 314

RESULT 7
Q65610
ID Q65610 PRELIMINARY; PRT; 233 AA.
AC Q65610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE N protein.
OS Kairi virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
OX NCBI_TaxID=80939;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94172333; PubMed=8126455;
RA Dunn E., Pritlove D.C., Elliott R.M.;
RT "Evolutionary relationships of the Bunyavirus S genome segment.";
RL J. Gen. Virol. 75:597-608 (1994).
DR EMBL; X73467; CAA51849.1; -.
DR GO; GO:0019013; C: viral nucleocapsid; IEA.
DR InterPro; IPR001784; Bunya_nucleocap.
DR Pfam; PF00952; Bunya_nucleocap; 1.
DR ProDom; PD001909; Bunya_nucleocap; 1.
SQ SEQUENCE 233 AA; 26578 MW; 3D34022413505CF6 CRC64;

Query Match 50.0%; Score 43; DB 2; Length 233;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
|:|:|:|:|:|:|:|:|:|
DB 182 RQRYNMLDASQWTKH 197

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RESULT 8
Q6BPY1
ID Q6BPY1 PRELIMINARY; PRT; 622 AA.
AC Q6BPY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to CA0631|IPF11698 Candida albicans IPF11698.
GN ORFNames=DEHA0E10450g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barray S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boiserame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382137; CAG87975.1; -.
SQ SEQUENCE 622 AA; 69830 MW; 423B43A5EB6A897D CRC64;

Query Match 50.0%; Score 43; DB 2; Length 622;
Best Local Similarity 60.0%; Pred. No. 76;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEA 15
|:|:|:|:|:|:|:|:|:|
DB 568 RHYLYNTDLDQDGA 582

RESULT 9
Q8IBC1
ID Q8IBC1 PRELIMINARY; PRT; 1916 AA.
AC Q8IBC1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein MAL8P1.11.
GN Name=MAL8P1.11;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAU51085.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1916 AA; 230013 MW; 68FF914B8A3519BD CRC64;

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Query Match      50.0%; Score 43; DB 2; Length 1916;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RORLYTDDAQOTE 14
   :|:|:|:|:|:|
DB 1299 KENYIYDGNETE 1312

RESULT 10
ID 045881 PRELIMINARY; PRT; 2225 AA.
AC 045881;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein W01F3.3.
GN ORFNames=W01F3.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Cummings P.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
DR EMBL; 292815; CAB07294.1; -.
DR PIR; T26063; T26063.
DR HSSP; P31713; 1SHP.
DR WormBase; WBGene00012186; W01F3.3.
DR WormPep; W01F3.3; C616531.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000716; Thyroglobulin_1.
DR InterPro; IPR006150; Worm repeat_1.
DR Pfam; PF00014; Kunitz BPTI; 10.
DR Pfam; PF00086; Thyroglobulin_1; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 10.
DR SMART; SM00211; TY; 1.
DR SMART; SM00289; WR1; 4.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 2225 AA; 242197 MW; A5DD8AE9D2A7B02A CRC64;

Query Match      50.0%; Score 43; DB 2; Length 2225;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
   :|:|:|:|:|:|
DB 477 QRYFYNDSQKE 489

RESULT 11
ID Q63KM0 PRELIMINARY; PRT; 660 AA.
AC Q63KM0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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DE Putative cysteine desulfurase.
GN ORFNames=BPSS1341;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., I.R.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tunapa S., Vesaratchaveit M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571966; CAH38812.1; -.
SQ SEQUENCE 660 AA; 68694 MW; AC6780F5CB5C33C CRC64;

Query Match      48.3%; Score 41.5; DB 2; Length 660;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 3 RYLTTDDAQOTEAH 16
   :|:|:|:|:|:|
DB 235 RY-FVDDAQPTNAH 247

RESULT 12
Q62CG0
ID Q62CG0 PRELIMINARY; PRT; 671 AA.
AC Q62CG0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cysteine desulfurase, putative.
GN ORFNames=BMAA0933;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA Sellengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251 (2004).
DR EMBL; CP000011; AAU46114.1; -.
SQ SEQUENCE 671 AA; 69821 MW; 59F9027C0176C088 CRC64;

Query Match      48.3%; Score 41.5; DB 2; Length 671;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 3 RYLTTDDAQOTEAH 16
   :|:|:|:|:|:|
DB 246 RY-FVDDAQPTNAH 258

RESULT 13

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P71428
ID P71428 PRELIMINARY; PRT; 93 AA.
AC P71428;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transposable element ISL1.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Group B;
RA MEDLINE=85295506; PubMed=2993817;
RA Shimizu-Kadota M., Kiwaki M., Hirokawa H., Tsuchida N.;
RT "ISL1: a new transposable element in Lactobacillus casei.";
RL Mol. Gen. Genet. 200:193-198(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Group B;
RA Shimizu-Kadota M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02734; CAA26516.1; -.
DR PIR; S28726; S28726.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF01527; Transposase_8; 1.
DR SEQUENCE 93 AA; 10745 MW; 62584573F7F83DCE CRC64;
SQ
Query Match 47.7%; Score 41; DB 2; Length 93;
Best Local Similarity 61.5%; Pred. NO. 20;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQT 13
Db 43 RWRKLYTDDGKQT 55

RESULT 14
Q7XAQ1 PRELIMINARY; PRT; 243 AA.
AC Q7XAQ1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MADS-box transcription factor.
GN Name=HCSF1;
OS Houttuynia cordata (Chameleon plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Piperales; Saururaceae;
OC Houttuynia.
OX NCBI_TaxID=16752;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito M., Imafuku M., Tanabe Y., Aoki S., Hasebe M.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AB089157; BAC80253.1; -.
DR HSPF; Q02078; IEGW.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.

DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 243 AA; 27728 MW; 7B34DBE4609D8B8 CRC64;

Query Match 47.7%; Score 41; DB 2; Length 243;
Best Local Similarity 50.0%; Pred. NO. 59;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQTEAH 16
Db 168 RRLQLDLDGSGQTNP 183

RESULT 15
O64468 PRELIMINARY; PRT; 349 AA.
AC O64468;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative GDSL-motif lipase/hydrolase.
GN Name=At2g19050;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Sonerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002392; AAD12023.1; -.
DR PIR; T00525; T00525.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hydrolase.
SQ SEQUENCE 349 AA; 38577 MW; 05DAC363EA5F3D2A CRC64;

Query Match 47.7%; Score 41; DB 2; Length 349;
Best Local Similarity 46.7%; Pred. NO. 90;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQTEA 15
Db 309 QRRVYWDNVHSTEA 323

Search completed: July 8, 2005, 22:18:04
Job time : 22.2667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:53:57 ; Search time 19.625 Seconds
(without alignments)
295.613 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89
Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	15	4	AAB68419
2	89	100.0	124	5	ABB81312
3	89	100.0	181	4	AAU00965
4	89	100.0	183	8	ADL57109
5	89	100.0	208	4	AAE05078
6	89	100.0	208	5	AAU83630
7	89	100.0	208	5	ABG32358
8	89	100.0	208	5	AAE17601
9	89	100.0	208	6	ABU80777
10	89	100.0	208	6	ABO33743
11	89	100.0	208	6	ABU82086
12	89	100.0	208	6	ABP96156
13	89	100.0	208	6	ABU72266
14	89	100.0	208	6	ABJ72394
15	89	100.0	208	6	ABO34289
16	89	100.0	208	7	ADA37038
17	89	100.0	208	7	ABJ72096
18	89	100.0	208	7	ABU883568
19	89	100.0	208	7	ABU80674
20	89	100.0	208	7	ABU73215
21	89	100.0	208	7	ABU78297
22	89	100.0	208	7	ABU84945
23	89	100.0	208	7	ABU78051
24	89	100.0	208	7	ABU87117
25	89	100.0	208	7	ADB84699

26	89	100.0	208	7	ADB83814	Novel hum
27	89	100.0	208	7	ADB72969	Novel hum
28	89	100.0	208	7	ADC36807	Human PRO
29	89	100.0	208	7	ADC21797	Human PRO
30	89	100.0	208	7	ADC49828	Novel hum
31	89	100.0	208	7	ADC49027	Novel hum
32	89	100.0	208	7	ADC49544	Novel hum
33	89	100.0	208	7	ADC47405	Novel hum
34	89	100.0	208	7	ADC47150	Novel hum
35	89	100.0	208	7	ADC78025	Novel hum
36	89	100.0	208	7	ADD06260	Novel hum
37	89	100.0	208	7	ADC77779	Novel hum
38	89	100.0	208	7	ADD50742	Novel hum
39	89	100.0	208	7	ADD50988	Novel hum
40	89	100.0	208	7	ADD50469	Human PRO
41	89	100.0	208	7	ADD50223	Human PRO
42	89	100.0	208	7	ADD51234	Novel hum
43	89	100.0	208	8	ADC48781	Novel hum
44	89	100.0	208	8	ADE20952	Novel hum
45	89	100.0	208	8	ADE05796	Human PRO

ALIGNMENTS

RESULT 1

AAB68419
ID AAB68419 standard; peptide; 15 AA.

AC AAB68419;

XX 23-JUL-2001 (first entry)

DE Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21).

XX Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation;
KW hepatic cell; cirrhosis; infertility; impotence; testicular cancer;
KW leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

OS Homo sapiens.

XX WO200136640-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031745.

XX 18-NOV-1999; 99US-0166540P.

PR 11-MAY-2000; 2000US-0203633P.

XX (CHIR) CHIRON CORP.

XX (KYOU) UNIV KYOTO.

PI Itoh N, Kavanaugh WM;

XX WPI; 2001-343823/36.

XX New nucleic acid molecule useful for treating disease, e.g. infertility,
impotence, or testicular cancer.

XX Claim 17; Page 40; 61pp; English.

PS The present sequence represents an epitope-bearing portion of human
XX fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and
XX differentiation of a variety of cell types. FGF-21 nucleic acids and
XX polypeptides are useful for treating diseases and disorders characterised
XX by inadequate numbers of hepatic cells, preferably cirrhosis of the
XX liver. They may also be used in the treatment of infertility, impotence,
XX and testicular cancer, as well as leukemia, lymphoma, autoimmune disease,
XX or proliferative disorders of the thymus

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
| | | | | | | | | | | | | | |
Db 1 HLPGNKSPHRDPAPR 15

RESULT 2
ABB81312
ID ABB81312 standard; protein; 124 AA.
XX
AC ABB81312;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human FGF21 core structure amino acid sequence.
XX
KW Fibroblast growth factor 9; FGF-9; cytostatic; vulnery; osteopathic;
KW antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder;
KW fibroblast growth factor receptor; cancer; bone fracture healing;
KW bone growth; wound healing; achondroplasia; hypochondroplasia;
KW osteoporosis; cartilage defect; multiple myeloma.
XX
OS Homo sapiens.
XX
WO200236732-A2.
XX
PD 10-MAY-2002.
XX
PF 18-OCT-2001; 2001WO-IL000962.
XX
PR 31-OCT-2000; 2000IL-00139380.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Bogin O, Adar R, Yayon A;
XX
WPI; 2002-479754/51.
XX
New variants of fibroblast growth factor, useful for treating skeletal
disorders including osteoporosis, malignancies and to enhance wound and
fracture healing.

Disclosure; Fig 1; 74pp; English.

The present invention describes an active variant (I) of a fibroblast
growth factor (FGF) having at least one mutation in the beta-8-beta-9
loop, having enhanced specificity for one receptor subtype compared to
the corresponding wild type FGF, by decreasing the biological activity
mediated by at least one receptor subtype while retaining the activity
mediated through another receptor subtype. (I) has cytostatic, vulnery,
osteopathic and antiarthritic activities. (I) can be used as a regulator
of vasculogenesis or angiogenesis. (I) is useful for preparing a
medicament and for treating a disease or disorder related to normal or
abnormal FGF receptors (FGFRs), especially skeletal disorders, cancer, to
enhance bone fracture healing or bone growth processes and wound healing
processes. (I) is useful in detection and treatment of various FGFR
related disorders including skeletal disorders e.g. achondroplasia,
hypochondroplasia, and osteoporosis, and cartilage defects, multiple
myeloma, epithelial cancers such as transitional cell carcinoma of the
bladder and cervical carcinoma. The novel mutants are useful in high
expression systems suitable for pharmaceutical production, targeting of
drugs or other agents to tissues and cells having specific FGFR subtypes,
and serve as template for the formation of improved agonists and
antagonists of FGFRs in various disorders such as skeletal disorders and
cancer. The present sequence represents a FGF core structure amino acid
sequence which is given in the exemplification of the present invention

Sequence 124 AA;
SQ

Query Match 100.0%; Score 89; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.4e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
| | | | | | | | | | | | | | |
Db 101 HLPGNKSPHRDPAPR 115

RESULT 3
AAU00965
ID AAU00965 standard; protein; 181 AA.
XX
AC AAU00965;
XX
DT 24-MAY-2001 (first entry)
XX
DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
XX
KW Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;
KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
KW multiple sclerosis; short stature; delayed maturation; excessive growth;
KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
KW androgen target organ abnormality; respiratory distress syndrome; stroke;
KW cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness;
KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
KW decreased stamina; decreased cardiac function; immune system dysfunction;
KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;
KW senile dementia; human.
XX
OS Homo sapiens.
XX
WO200118172-A2.
XX
PD 15-MAR-2001.
XX
PF 05-SEP-2000; 2000WO-US024373.
XX
PR 07-SEP-1999; 99US-00391861.
XX
PR 23-AUG-2000; 2000US-00644052.
XX
PA (AMGE-) AMGEN INC.
XX
PI Thomson AR, Liu B;
XX
WPI; 2001-226743/23.
XX
Novel isolated fibroblast growth factor-like polypeptide useful for
treating, preventing or ameliorating cirrhosis, inflammatory bowel
disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
osteoporosis.

Claim 14; Page 116-117; 138pp; English.

The sequence represents a fragment of a fibroblast growth factor-like
(FGF-like) polypeptide. FGF-like protein and its associated nucleic acid
play a role in modulating body growth, maturation or life-span. They are
also useful for treating, preventing or ameliorating disorders such as
cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,
diabetes, obesity, gastrointestinal abnormalities, neurodegenerative
diseases, damage to renal tubules as a result of acute tubular necrosis,
haematopoietic cell reconstruction following chemotherapy, wasting
syndromes (e.g., cancer associated cachexia), damage to the corneal
epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
stature, delayed maturation, excessive growth (e.g. acromegaly),
premature maturation, alopecia, abnormalities of androgen target organs,
bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
of the eye or other tissues, atherosclerosis, hypercholesterolemia,
stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
baldness, wrinkles, increased fatigue, decreased stamina, decreased
cardiac function, immune system dysfunction, cancer, Parkinson's disease,

CC senile dementia, Alzheimer's disease, and decreased cognitive function
 XX Sequence 181 AA;
 SQ

Query Match 100.0%; Score 89; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 Db 117 HLPGNKSPHRDPAPR 131
 |||||

RESULT 4
 ADL57109
 ID ADL57109 standard; protein; 183 AA.
 AC ADL57109;
 DT 03-JUN-2004 (first entry)
 DE Human NOV6a protein SEQ ID NO:54.
 KW human; antidiabetic; anorectic; cardiant; hypotensive;
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
 KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
 KW dermatological; antiasthmatic; antilipaeamic; gene therapy;
 KW fibroblast growth factor receptor 4; FGFR4;
 KW complement factor I precursor; matrix metalloproteinase-15 precursor;
 KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
 KW fibroblast growth factor-21; FGF-21;
 KW alpha-2 macroglobulin-like polypeptide variant;
 KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
 KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
 XX Homo sapiens.
 OS
 XX
 XX WO2004022723-A2.
 XX
 XX 18-MAR-2004.
 XX
 XX 09-SEP-2003; 2003WO-US028141.
 XX
 XX 09-SEP-2002; 2002US-0409145P.
 XX 10-SEP-2002; 2002US-0409544P.
 XX 12-SEP-2002; 2002US-0410320P.
 XX 16-SEP-2002; 2002US-0411060P.
 XX 23-SEP-2002; 2002US-0412766P.
 XX 23-SEP-2002; 2002US-0412825P.
 XX 24-SEP-2002; 2002US-0412767P.
 XX 25-SEP-2002; 2002US-0413342P.
 XX 30-SEP-2002; 2002US-0414832P.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Zhong M, Guo X, Anderson DW, Ort T, Padigar M, Rieger DK;
 XX WPI, 2004-315567/29.
 XX N-PSDB; ADL57108.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
 XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 XX asthma, or infections.
 XX
 XX Claim 1; SEQ ID NO 54; 214pp; English.
 XX
 XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
 XX mature form of any of the 37 amino acid sequences fully defined in the
 XX specification. A polypeptide of the invention has antidiabetic,
 XX anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
 XX virucide, antibacterial, fungicide, protozoacide, nootropic,

CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
 CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
 CC antilipaeamic activity. A polynucleotide of the invention may have a use
 CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
 CC are useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOVX-associated disorder.
 CC The nucleic acid molecules, polypeptides and antibodies are useful for
 CC treating, preventing or diagnosing diseases such as metabolic disorders,
 CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
 CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
 CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
 CC disease, Parkinson's disease, epilepsy, immune disorders
 CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
 CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridisation probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
 CC polypeptides of the invention show homology to certain known human
 CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
 CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
 CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
 CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
 CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
 CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
 CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
 CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
 CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
 CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
 CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
 CC of the invention.
 XX
 XX Sequence 183 AA;
 SQ

Query Match 100.0%; Score 89; DB 8; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 Db 117 HLPGNKSPHRDPAPR 131
 |||||

RESULT 5
 AA05078
 ID AA05078 standard; protein; 208 AA.
 XX
 XX AA05078;
 XX
 XX 18-SEP-2001 (first entry)
 XX
 XX Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
 XX
 XX Human fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;
 XX proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis;
 XX chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture;
 XX bone formation; diabetes mellitus; neural cell development; angiogenesis;
 XX amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer;
 XX congenital disorder; wound healing; cardiac function; glomerulonephritis;
 XX surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
 XX hypertension; cytostatic; vasotropic; therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..27
 XX Protein 28..208
 XX Binding-site 44..46
 XX /label= Signal_peptide
 XX /label= Human_mature_zFGF11_protein

```

FT  /note= "Heparin binding domain"
XX  WO2000149849-A1.
XX  12-JUL-2001.
XX
XX  05-JAN-2001; 2001WO-US000324.
XX
XX  05-JAN-2000; 2000US-00477886.
XX
XX  (ZYMO ) ZYMOGENETICS INC.
XX
XX  Conklin DC, Chen Z;
XX
XX  WPI; 2001-441880/47.
XX  N-PSDB; NAD09151.
XX
XX  Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast
XX  growth factor family, for stimulating proliferation of mesenchymal,
XX  osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
XX  cancer.
XX
XX  Claim 1; Page 63; 69pp; English.
XX
XX  The present sequence is human fibroblast growth factor (FGF) homologue,
XX  zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
XX  for stimulating proliferation of mesenchymal cells, osteoblastic lineage
XX  cells. zFGF11 is useful for identifying chromosomal disorders associated
XX  with abnormal expression of zFGF11 protein. zFGF11 is also useful for
XX  stimulation, inhibition or proliferation of myocytes, smooth muscle
XX  cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
XX  crest stem cells and neuronal progenitors, pancreatic cells, prostate-
XX  derived cells and endothelial cells and inhibiting chondrosarcomas,
XX  atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
XX  results in bone formation useful for treating bone defects, fractures,
XX  osteoporosis and other deficiencies in bone structure and formation.
XX  zFGF11 is useful for treating disorders associated with diabetes
XX  mellitus, neural cell development or degeneration, amyotrophic lateral
XX  sclerosis, cerebrovascular stroke, neuropathy associated with lack of
XX  maintenance of neuronal differentiation and congenital disorders of the
XX  nervous system or lack of neuronal development, promoting angiogenesis
XX  and wound healing, for revascularisation in eye, complications related to
XX  poor circulation such as diabetic foot ulcers, improving cardiac
XX  function, modulating surfactant production in the lung epithelium, to
XX  reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
XX  events, particularly in the heart or brain and for inducing skeletal
XX  muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
XX  treating of systemic and pulmonary hypertension. Antagonists of zFGF11
XX  are useful for inhibiting disorders associated with kidney epithelium
XX  such as glomerulonephritis
XX
XX  Query Match          100.0%; Score 89; DB 4; Length 208;
XX  Best Local Similarity 100.0%; Pred. No. 0.00012;
XX  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 HLPGNKSPHRDPAPR 15
XX    |||||
XX  Db 144 HLPGNKSPHRDPAPR 158
XX
XX  RESULT 6
XX  AAU83630
XX  ID AAU83630 standard; protein; 208 AA.
XX
XX  AC AAU83630;
XX
XX  DT 08-MAY-2002 (first entry)
XX
XX  DE Human PRO protein, Seq ID No 78.
XX
XX  KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

```

```

KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX Homo sapiens.
XX OS
XX PN WO200208288-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 29-JUN-2001; 2001WO-US021066.
XX
XX PR 20-JUL-2000; 2000US-0219556P.
XX PR 25-JUL-2000; 2000US-0220585P.
XX PR 25-JUL-2000; 2000US-0220605P.
XX PR 25-JUL-2000; 2000US-0220607P.
XX PR 25-JUL-2000; 2000US-0220624P.
XX PR 25-JUL-2000; 2000US-0220638P.
XX PR 25-JUL-2000; 2000US-0220664P.
XX PR 25-JUL-2000; 2000US-0220666P.
XX PR 26-JUL-2000; 2000US-0220893P.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 01-AUG-2000; 2000US-0222425P.
XX PR 22-AUG-2000; 2000US-0227133P.
XX PR 23-AUG-2000; 2000WO-US023522.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 10-NOV-2000; 2000WO-US030873.
XX PR 28-NOV-2000; 2000US-0253646P.
XX PR 01-DEC-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-00747259.
XX PR 28-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2001; 2001WO-US006666.
XX PR 12-MAR-2001; 2001US-00816744.
XX PR 10-MAY-2001; 2001US-00854208.
XX PR 10-MAY-2001; 2001US-00854280.
XX PR 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
XX N-PSDB; ASK33574.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumors such
XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX or liver tumor.
XX
XX Claim 11; Fig 78; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumors, especially lung
XX cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
XX liver tumor. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention
XX
XX Sequence 208 AA;
XX
XX Query Match          100.0%; Score 89; DB 5; Length 208;

```

Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
|||||
DB 144 HLPGNKSPHRDPAPR 158

RESULT 7
ABG32358
ID ABG32358 standard; protein; 208 AA.
XX AC ABG32358;
XX DT 05-NOV-2002 (first entry)
XX DE Human fibroblast growth factor (FGF) homologue, zFGF11.
XX KW Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFRIIIC;
KW osteoblastic lineage cell; diabetes mellitus; neuropathy;
KW neural cell development; amytrophic lateral sclerosis;
KW cerebrovascular stroke; neuronal differentiation; congenital disorder;
KW nervous system disorder; cardiac function; wound healing.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Signal_sequence
FT Protein 28..208
FT /note= "Mature fibroblast growth factor homologue,
zFGF11. This sequence is specifically claimed in claim 4"

US2002081663-A1.
27-JUN-2002.
05-JAN-2001; 2001US-00755695.
05-JAN-2000; 2000US-0174526P.
(CONK/) CONKLIN D C.
(CHEN/) CHEN Z.
Conklin DC, Chen Z;
WPI: 2002-626540/67.
N-PSDB; ABK91310.
Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amytrophic lateral sclerosis, cerebrovascular stroke.
Claim 4; Fig 1; 35pp; English.
The invention relates to an isolated human polypeptide (I) for zFGF11 (a fibroblast growth factor), and the encoding polynucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of FGFRIIIC in a biological sample and stimulating proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amytrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation, and congenital disorders of the nervous system or lack of neuronal development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidermis. The present sequence represents the amino acid sequence of human zFGF11
Sequence 208 AA;

Query Match 100.0%; Score 89; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
|||||
DB 144 HLPGNKSPHRDPAPR 158

RESULT 8
AAE17601
ID AAE17601 standard; protein; 208 AA.
XX AC AAE17601;
XX DT 22-APR-2002 (first entry)
XX DE Human extracellular messenger (XMES)-3 protein.
XX KW Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;
KW Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
KW developmental disorder; anemia; Cushing's syndrome; endocrine disorder;
KW vascular malformation; cell proliferative disorder; gene therapy; cancer;
KW neuroprotective; trauma; hypopituitarism; hypothyroidism; antiheilmithic;
KW hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic;
KW diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
KW antiviral; antifungal; parasitic; protozoal; allergy.
XX OS Homo sapiens.
XX FN WO200194587-A2.
XX PD 13-DEC-2001.
XX PF 06-JUN-2001; 2001WO-US018476.
XX PR 06-JUN-2000; 2000US-0210233P.
PR 23-JUN-2000; 2000US-0213465P.
PR 14-NOV-2000; 2000US-0249019P.
XX (INCY-) INCYTE GENOMICS INC.
XX PA Lal P, Yue H, He A, Nguyen DB, Walia N, Gandhi AR, Azimzal Y;
PI Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
PI Policky JL;
XX WPI: 2002-154573/20.
DR N-PSDB; AAD28493.
XX New extracellular messenger polypeptides and polynucleotides encoding them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders.
XX PS Claim 1; Page 111; 123pp; English.
XX The present invention relates to new extracellular messenger polypeptides and polynucleotides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. acquired immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy, aneurysm or vascular malformation), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypopituitarism, hypothyroidism, hyperthyroidism or gonadal steroid hormones, and pancreatic disorders such as type I or type II diabetes mellitus. The XMES may be used for somatic or germline gene therapy. The present

```

CC sequence is human XMES-3 protein
XX
SQ Sequence 208 AA;

Query Match      100.0%; Score 89; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
   |||||
DB 144 HLPGNKSPHRDPAPR 158

RESULT 9
ABU80777
ID ABU80777 standard; protein; 208 AA.
XX
AC ABU80777;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #39.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
OS Homo sapiens.
XX
FN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-342045/32.
DR N-PSDB; ACA66879.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipdIDEntry.html
XX
SQ Sequence 208 AA;

Query Match      100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
   |||||
DB 144 HLPGNKSPHRDPAPR 158

RESULT 10
ABO33743
ID ABO33743 standard; protein; 208 AA.
XX
AC ABO33743;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioeffector; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
XX
OS Homo sapiens.
XX
FN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR N-PSDB; ACD68631.
XX
PT New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any of these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioeffectors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

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XX Sequence 208 AA;
SQ Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158

RESULT 11
ABU82086
ID ABU82086 standard; protein; 208 AA.
XX AC
XX ABU82086;
XX DT
XX 25-JUN-2003 (first entry)
XX DE
XX Novel human secreted and transmembrane protein PRO10196.
XX KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
XX KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
XX KW gene therapy; cardiovascular disorder; endothelial disorder;
XX KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
XX KW age-related macular degeneration; atherosclerosis; hypertension;
XX KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
XX KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
XX KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX OS Homo sapiens.
XX FN US2003088063-A1.
XX PD 08-MAY-2003.
XX PF 12-AUG-2002; 2002US-00219003.
XX PR 25-JUL-2000; 2000US-0220664P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX DR WPI; 2003-393229/37.
XX DR N-PSDB; ACA68535.
XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX PT infarction), endothelial or angiogenic disorders in a mammal.
XX PS Claim 11; Fig 78; 314pp; English.
XX CC The invention describes one hundred and eighty seven nucleic acids
XX CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
XX CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
XX CC treating or diagnosing a cardiovascular, endothelial or angiogenic
XX CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
XX CC related macular degeneration, atherosclerosis, hypertension, arterial
XX CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
XX CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
XX CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
XX CC have applications in molecular biology, including use as hybridisation
XX CC probes, and in chromosome and gene mapping. This is the amino acid
XX CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158

RESULT 12
ABP96156
ID ABP96156 standard; protein; 208 AA.
XX AC
XX ABP96156;
XX DT
XX 12-MAY-2003 (first entry)
XX DE
XX Human fibroblast growth factor 21 protein SEQ ID NO:2.
XX KW Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter;
XX KW diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;
XX KW type 1 diabetes.
XX OS Homo sapiens.
XX FN WO2003011213-A2.
XX PD 13-FEB-2003.
XX PF 22-JUL-2002; 2002WO-US021290.
XX PR 30-JUL-2001; 2001US-0308702P.
XX PR 10-JAN-2002; 2002US-0347991P.
XX PA (ELIL ) LILLY & CO ELI.
XX PI Glasebrook AL, Hammond LJ, Kharitonkov A, Shivanova TL;
XX DR WPI; 2003-248106/24.
XX DR N-PSDB; ABZ79797.
XX PT Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or
XX PT obesity, by administering composition comprising fibroblast growth factor
XX PT -21.
XX PS Claim 3; Fig 1; 32pp; English.
XX CC The present sequence represents human fibroblast growth factor 21 (FGF-
XX CC 21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
XX CC qter. The present invention describes a method for treating a mammal
XX CC exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for
XX CC obesity which comprises administering to the mammal a composition
XX CC comprising FGF-21 which has at least 95% amino acid sequence identity to
XX CC the 208 amino acid sequence given in ABP96156. Also described: (1)
XX CC inducing an increase in glucose uptake in adipocyte cells by
XX CC administering FGF-21 to induce an increase in glucose uptake; and (2)
XX CC or obesity in a mammal using FGF-21 having 95% amino acid sequence
XX CC identity to ABP96156. FGF-21 has antidiabetic and anorectic activities.
XX CC The method is useful for treating a mammal exhibiting type 2 or 1
XX CC diabetes or for treating a mammal for obesity. The method is preferably
XX CC useful for treating humans exhibiting type 1 or type 2 diabetes, and for
XX CC treating domestic animals for obesity
XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
```

RESULT 13
ABJ72266
ID ABJ72266 standard; protein; 208 AA.

AC ABJ72266;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10196 protein.

XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.

OS Homo sapiens.

XX US2003050448-A1.

XX 13-MAR-2003.

XX 28-AUG-2002; 2002US-00230414.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-521818/49.

XX N-PSDB; ABT44264.

XX New nucleic acid encoding for a PRO protein, useful for the manufacture
XX of a medicament for diagnosing or treating tumors or for measuring or
XX detecting expression of an associated gene.

XX Claim 11; Fig 78; 315pp; English.

XX The invention relates to a novel isolated nucleic acid encoding a fully
XX defined PRO polypeptide. The molecules of the invention may be useful for
XX stimulating proliferation or gene expression in pericyte cells or the
XX release of TNF-alpha from human blood. Other possible uses include the
XX stimulation or inhibition of chondrocyte proliferation or
XX differentiation and the stimulation of human dermal fibroblast cell
XX proliferation and the detection of the presence of a tumour within a
XX mammal. Furthermore, the nucleic acid may be useful for the manufacture
XX of a medicament for diagnosing or treating a tumour within a mammal or
XX as for measuring or detecting the expression of an associated gene, as well
XX as during gene therapy. The current sequence is that of the human PRO
XX protein of the invention

XX Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLPGNKSPHRDPAPR 15
|||
Db 144 HLPGNKSPHRDPAPR 158

RESULT 14
ABJ72394
ID ABJ72394 standard; protein; 208 AA.

XX ABJ72394;

XX 06-NOV-2003 (first entry)

XX

DE Human PRO10196 protein.

XX PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.

XX Homo sapiens.

XX US2003027988-A1.

XX 06-FEB-2003.

XX 26-AUG-2002; 2002US-00227884.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-503301/47.

XX N-PSDB; ABT44547.

XX New PRO protein encoding nucleic acid, useful for preparing PRO
XX polypeptides and anti-PRO antibodies for detecting the presence of a
XX tumor in a mammal.

XX Claim 11; Fig 78; 324pp; English.

XX The invention relates to a novel isolated PRO protein encoding nucleic
XX acid. The nucleic acid of the invention may be useful for preparing PRO
XX polypeptides and anti-PRO antibodies for detecting the presence of a
XX tumour in a mammal. Furthermore, the molecules of the invention may be
XX useful for stimulating proliferation or gene expression in pericyte
XX cells, the release of tumour necrosis factor (TNF)-alpha from human
XX blood, the proliferation or differentiation of chondrocyte cells and for
XX inhibiting the proliferation of normal human dermal fibroblast cells.
XX Finally, the molecules may be utilised during gene therapy. The current
XX sequence is that of the human PRO protein of the invention

XX Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLPGNKSPHRDPAPR 15
|||
Db 144 HLPGNKSPHRDPAPR 158

RESULT 15
ABO34289
ID ABO34289 standard; protein; 208 AA.

XX ABO34289;

XX 19-SEP-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO 10196.

XX Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.

XX Homo sapiens.

XX US200304934-A1.

XX 06-MAR-2003.

XX 28-AUG-2002; 2002US-00230338.
PF 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI WPI; 2003-492274/46.
XX DR N-PSDB; ACD82214.
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX Claim 19; Fig 78; 315pp; English.
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. Nucleic acids that encode PRO can be used to generate either
CC transgenic animals or knock-out animals useful in developing and
CC screening of therapeutically useful reagents. The nucleic acids may also
CC be used in gene therapy for replacing defective gene, in chromosome
CC identification, as chromosome markers, or in generating probes to isolate
CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
CC and for detecting the presence of tumour in an mammal. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
XX of a human secreted/transmembrane PRO polypeptide
SQ Sequence 208 AA;
Query Match . 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPAPR 15
|||||
Db 144 HLPGNKSPHRDPAPR 158

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Job time : 19.625 secs

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OM protein - protein search, using sw model

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(without alignments)
324.193 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

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Total number of hits satisfying chosen parameters: 1726216

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	15	13 US-10-060-765-8	Sequence 8, Appli
2	89	100.0	15	16 US-10-818-140-8	Sequence 8, Appli
3	89	100.0	15	17 US-10-771-173-8	Sequence 8, Appli
4	89	100.0	68	9 US-09-801-968-36	Sequence 36, Appli
5	89	100.0	68	10 US-09-802-154-36	Sequence 36, Appli
6	89	100.0	136	9 US-09-901-938-33	Sequence 33, Appli
7	89	100.0	136	14 US-10-379-334-33	Sequence 33, Appli
8	89	100.0	183	17 US-10-659-004-54	Sequence 54, Appli
9	89	100.0	208	9 US-09-755-695-2	Sequence 2, Appli
10	89	100.0	208	14 US-10-227-884-78	Sequence 78, Appli
11	89	100.0	208	14 US-10-230-163-78	Sequence 78, Appli

12	89	100.0	208	14	US-10-230-338-78	Sequence 78, Appli
13	89	100.0	208	14	US-10-218-631-78	Sequence 78, Appli
14	89	100.0	208	14	US-10-230-414-78	Sequence 78, Appli
15	89	100.0	208	14	US-10-232-224-78	Sequence 78, Appli
16	89	100.0	208	14	US-10-216-159A-78	Sequence 78, Appli
17	89	100.0	208	14	US-10-218-849-78	Sequence 78, Appli
18	89	100.0	208	14	US-10-227-873-78	Sequence 78, Appli
19	89	100.0	208	14	US-10-227-883-78	Sequence 78, Appli
20	89	100.0	208	14	US-10-219-076-78	Sequence 78, Appli
21	89	100.0	208	14	US-10-230-434-78	Sequence 78, Appli
22	89	100.0	208	14	US-10-219-003-78	Sequence 78, Appli
23	89	100.0	208	14	US-10-219-075-78	Sequence 78, Appli
24	89	100.0	208	14	US-10-219-464-78	Sequence 78, Appli
25	89	100.0	208	14	US-10-219-466-78	Sequence 78, Appli
26	89	100.0	208	14	US-10-219-479-78	Sequence 78, Appli
27	89	100.0	208	14	US-10-219-481-78	Sequence 78, Appli
28	89	100.0	208	14	US-10-230-260-78	Sequence 78, Appli
29	89	100.0	208	14	US-10-232-231-78	Sequence 78, Appli
30	89	100.0	208	14	US-10-232-233-78	Sequence 78, Appli
31	89	100.0	208	14	US-10-216-165-78	Sequence 78, Appli
32	89	100.0	208	14	US-10-218-956-78	Sequence 78, Appli
33	89	100.0	208	14	US-10-219-468-78	Sequence 78, Appli
34	89	100.0	208	14	US-10-219-478-78	Sequence 78, Appli
35	89	100.0	208	14	US-10-219-536-78	Sequence 78, Appli
36	89	100.0	208	14	US-10-233-205-78	Sequence 78, Appli
37	89	100.0	208	14	US-10-219-072-78	Sequence 78, Appli
38	89	100.0	208	14	US-10-219-470-78	Sequence 78, Appli
39	89	100.0	208	14	US-10-219-474-78	Sequence 78, Appli
40	89	100.0	208	14	US-10-219-524-78	Sequence 78, Appli
41	89	100.0	208	14	US-10-219-528-78	Sequence 78, Appli
42	89	100.0	208	14	US-10-227-880-78	Sequence 78, Appli
43	89	100.0	208	14	US-10-227-881-78	Sequence 78, Appli
44	89	100.0	208	14	US-10-227-882-78	Sequence 78, Appli
45	89	100.0	208	14	US-10-230-436-78	Sequence 78, Appli

ALIGNMENTS

RESULT 1
US-10-060-765-8
; Sequence 8, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060.765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-8

Query Match 100.0%; Score 89; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 1 HLPGNKSPHRDPAPR 15

RESULT 2

US-10-818-140-8
; Sequence 8, Application US/10818140

Db 107 HLPGNKSPHRDPAPR 121

RESULT 7
US-10-379-334-33
; Sequence 33, Application US/10379334
; Publication No. US20030181379A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/10/379,334
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/901,938
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-379-334-33

Query Match 100.0%; Score 89; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 HLPGNKSPHRDPAPR 15
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Db 107 HLPGNKSPHRDPAPR 121

RESULT 8
US-10-659-004-54
; Sequence 54, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 183
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-659-004-54

Query Match 100.0%; Score 89; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
|||||

Db 117 HLPGNKSPHRDPAPR 131

RESULT 9
US-09-755-695-2
; Sequence 2, Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; FILE REFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09/755,695
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/174,526
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2

Query Match 100.0%; Score 89; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 HLPGNKSPHRDPAPR 15
|||||

Db 144 HLPGNKSPHRDPAPR 158

RESULT 10
US-10-227-884-78
; Sequence 78, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31

مر

;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1998-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1998-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1998-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1998-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/149638
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1998-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1998-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1998-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1998-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1998-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15

DB 144 HLPGNKSPHRDPAPR 158

RESULT 11

US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656

;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/081819
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;; PRIOR APPLICATION NUMBER: 60/090557
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095318
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;; PRIOR APPLICATION NUMBER: 60/099596
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;; PRIOR APPLICATION NUMBER: 60/099803
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; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/106905
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; PRIOR APPLICATION NUMBER: 60/108787
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; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222

; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158
|||||||
|||||||

RESULT 12
US-10-230-338-78
; Sequence 78, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 13
US-10-218-631-78
; Sequence 78, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 14
US-10-230-414-78
; Sequence 78, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

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Search completed: July 8, 2005, 22:44:50
Job time : 17.875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 22:04:53 ; Search time 5.0625 Seconds
(without alignments)
221.182 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	89	100.0	15	4	US-09-715-805-8
2	89	100.0	181	4	US-09-390-207-5
3	89	100.0	209	4	US-09-390-207-2
4	89	100.0	209	4	US-09-715-805-4
5	57	64.0	1419	4	US-09-252-991A-31822
6	51	57.3	133	4	US-09-252-991A-22856
7	51	57.3	187	4	US-09-252-991A-18109
8	46	51.7	286	4	US-09-252-991A-29952
9	46	51.7	307	4	US-09-252-991A-21588
10	46	51.7	330	4	US-09-252-991A-25664
11	46	51.7	392	4	US-09-270-767-35161
12	46	51.7	392	4	US-09-270-767-50378
13	45	50.6	209	4	US-09-252-991A-30648
14	45	50.6	601	4	US-09-252-991A-23280
15	45	50.6	632	4	US-09-252-991A-24235
16	45	50.6	689	4	US-09-949-016-11276
17	45	50.6	1294	2	US-08-819-288-3
18	45	50.6	1294	3	US-09-400-348-3
19	45	50.6	1321	1	US-08-261-822A-3
20	45	50.6	1321	5	PCT-US95-07744A-3
21	44.5	50.0	372	4	US-09-252-991A-32717
22	44.5	50.0	545	4	US-09-538-092-59
23	44	49.4	372	4	US-09-252-991A-23226
24	44	49.4	441	4	US-09-252-991A-27502
25	44	49.4	490	4	US-09-488-039A-8325
26	44	49.4	552	1	US-07-999-280A-22
27	44	49.4	552	1	US-07-999-280A-24

28	44	49.4	552	1	US-08-426-279-22	Sequence 22, Appl
29	44	49.4	552	1	US-08-426-279-24	Sequence 24, Appl
30	44	49.4	552	1	US-08-401-013-22	Sequence 22, Appl
31	44	49.4	552	1	US-08-401-013-24	Sequence 24, Appl
32	44	49.4	552	3	US-08-426-570-22	Sequence 22, Appl
33	44	49.4	552	3	US-08-426-570-24	Sequence 24, Appl
34	44	49.4	552	3	US-08-426-876-22	Sequence 22, Appl
35	44	49.4	552	3	US-08-426-876-24	Sequence 24, Appl
36	44	49.4	552	3	US-08-426-243-22	Sequence 22, Appl
37	44	49.4	552	3	US-08-426-243-24	Sequence 24, Appl
38	44	49.4	552	3	US-08-401-632-22	Sequence 22, Appl
39	44	49.4	552	3	US-08-401-632-24	Sequence 24, Appl
40	44	49.4	969	4	US-09-252-991A-26118	Sequence 26118, A
41	43	48.3	172	4	US-09-252-991A-22814	Sequence 22814, A
42	42	48.3	247	4	US-09-252-991A-22135	Sequence 22135, A
43	43	48.3	356	4	US-09-252-991A-26571	Sequence 26571, A
44	43	48.3	404	4	US-09-949-016-7963	Sequence 7963, Ap
45	43	48.3	410	1	US-08-123-343A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-715-805-8
; Sequence 8, Application US/09715805
; Patent No. 6716626
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. 6716626uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/09/715.805
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-715-805-8

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HLPGNKSPHRDPAPR 15
Db	1	HLPGNKSPHRDPAPR 15

RESULT 2

US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390.207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match 100.0%; Score 89; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 117 HLPGNKSPHRDPAPR 131

RESULT 3

US-09-390-207-2

; Sequence 2, Application US/09390207

; Patent No. 6504530

; GENERAL INFORMATION:

; APPLICANT: Thomason, Arlen

; APPLICANT: Liu, Benxian

; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides

; FILE REFERENCE: 99-371

; CURRENT APPLICATION NUMBER: US/09/390,207

; CURRENT FILING DATE: 1999-09-07

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-390-207-2

Query Match 100.0%; Score 89; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 8.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 145 HLPGNKSPHRDPAPR 159

RESULT 4

US-09-715-805-4

; Sequence 4, Application US/09715805

; Patent No. 6716626

; GENERAL INFORMATION:

; APPLICANT: Itoh, No. 6716626uyuki

; APPLICANT: Kavanaugh, W. Michael

; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION

; TITLE OF INVENTION: PRODUCTS

; FILE REFERENCE: PP-16758.001/201130.408

; CURRENT APPLICATION NUMBER: US/09/715,805

; CURRENT FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-715-805-4

Query Match 100.0%; Score 89; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 8.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 145 HLPGNKSPHRDPAPR 159

RESULT 5

US-09-252-991A-31822

; Sequence 31822, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 31822

; LENGTH: 1419

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31822

Query Match 64.0%; Score 57; DB 4; Length 1419;

Best Local Similarity 66.7%; Pred. No. 3.5;

Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 25 HLPRAQPHRRPAPR 39

RESULT 6

US-09-252-991A-22856

; Sequence 22856, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22856

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22856

Query Match 57.3%; Score 51; DB 4; Length 133;

Best Local Similarity 58.8%; Pred. No. 2.1;

Matches 10; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 1 HLPGN--KSPHRDPAPR 15

Db 109 HRPCTAASEPHRRPAPR 125

RESULT 7

US-09-252-991A-18109

; Sequence 18109, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18109

; LENGTH: 187

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18109

Query Match 57.3%; Score 51; DB 4; Length 187;
Best Local Similarity 57.1%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAP 14
Db 89 HRPGRHRHDPAP 102

RESULT 8

US-09-252-991A-29952
; Sequence 29952, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29952
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29952

Query Match 51.7%; Score 46; DB 4; Length 286;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAP 15
Db 35 HLPDRADPRADPR 49

RESULT 9

US-09-252-991A-21588
; Sequence 21588, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21588
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21588

Query Match 51.7%; Score 46; DB 4; Length 307;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGKNSPHRDPA 15
Db 100 PGDRPPGRPR 112

RESULT 10

US-09-252-991A-25664
; Sequence 25664, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25664
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25664

Query Match 51.7%; Score 46; DB 4; Length 330;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PGKNSPHRDPA 15
Db 5 PAGRRHRQPQR 17

RESULT 11

US-09-270-767-35161
; Sequence 35161, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35161
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35161

Query Match 51.7%; Score 46; DB 4; Length 392;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDPA 13
Db 303 LPGNRWPYRGPA 314

RESULT 12

US-09-270-767-50378
; Sequence 50378, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50378

; LENGTH: 392
; TYPE: PRT

; ORGANISM: Drosophila melanogaster
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50378

Query Match 51.7%; Score 46; DB 4; Length 392;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDPA 13
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Db 303 LFGNRWYRGPA 314

RESULT 13

US-09-252-991A-30648
; Sequence 30648, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30648

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30648

Query Match 50.6%; Score 45; DB 4; Length 209;
Best Local Similarity 58.3%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGKNSPHRDPA 14
|||:|:|:
Db 81 PGRATHPDPA 92

RESULT 14

US-09-252-991A-23280

; Sequence 23280, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 23280

; LENGTH: 601

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23280

Query Match 50.6%; Score 45; DB 4; Length 601;
Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
|||:|:|:
Db 359 HLPDRAHRRRRPAPQ 373

RESULT 15

US-09-252-991A-24235

; Sequence 24235, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 24235

; LENGTH: 632

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24235

Query Match 50.6%; Score 45; DB 4; Length 632;
Best Local Similarity 53.3%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
|||:|:|:
Db 16 HLPAGAADHAPPAPR 30

Search completed: July 8, 2005, 22:22:34
Job time : 6.0625 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:53:57 ; Search time 273.442 Seconds
(without alignments)
295.613 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 1113
Sequence: 1 MDSRTGPEHSLVWSVLG.....SSDPLSMVGPQGRSPSYAS 209

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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5: Geneseqp2002s:*

6: Geneseqp2003s:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	209	4	AAG65667 Human fib
2	1113	100.0	209	4	AAB68417 Amino aci
3	1113	100.0	209	5	AUU79289 Human FGF
4	1113	100.0	209	5	AAE18826 Human FGF
5	1113	100.0	209	8	ADM94766 Human fib
6	1109	99.6	209	8	ADL57117 Human NOV
7	1109	99.6	209	8	ADL57121 Human NOV
8	1108	99.6	209	8	ADL57125 Human NOV
9	1107	99.5	209	8	ADL57123 Human NOV
10	1107	99.5	209	8	ADL57127 Human NOV
11	1107	99.5	209	8	ADL57129 Human NOV
12	1106	99.4	209	4	AAB82351 Human JAF
13	1106	99.4	209	4	AAU00957 Human Fib
14	1106	99.4	209	4	AAB83951 Amino aci
15	1106	99.4	209	8	ADL57111 Human NOV
16	1106	99.4	209	8	ADL57113 Human NOV
17	1106	99.4	209	8	ADL57119 Human NOV
18	1098.5	98.7	208	4	AAE05078 Human fib
19	1098.5	98.7	208	5	AAU83630 Human PRO
20	1098.5	98.7	208	5	ABG32358 Human fib
21	1098.5	98.7	208	5	AAE17601 Human ext
22	1098.5	98.7	208	6	ABU80777 Human PRO
23	1098.5	98.7	208	6	ABO33743 Human hum
24	1098.5	98.7	208	6	ABU82086 Novel hum
25	1098.5	98.7	208	6	ABP96156 Human fib

ALIGNMENTS

RESULT 1

AAG65667

ID AAG65667 standard; protein; 209 AA.

AC AAG65667;

XX 07-JAN-2002 (first entry)

XX Human fibroblast growth factor (FGF)-21.

XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic; fat deposition; vulnery; antitumor; dermatological; anorectic; antidiabetic; antiinflammatory; cytostatic; hepatic; virucide; neuroprotectant; pulmonary; gene therapy; vaccine; human.

XX Homo sapiens.

XX WO200172957-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-IB000664.

XX 31-MAR-2000; 2000US-00540118.

XX (ITOH/) ITOH N.

XX Itch N;

XX WPI; 2001-611623/70.

XX New human nucleic acid encoding fibroblast growth factor-like peptide, useful for treatment and diagnosis of e.g. wounds and inflammatory bowel disease.

XX Disclosure; Fig 3; 172pp; English.

XX The invention provides human nucleic acids encoding fibroblast growth factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by standard recombinant methodology and are mitogenic for a wide range of cells, inducing differentiation and proliferation, and inhibiting deposition of fat. The FGF-like polypeptides, polynucleotides and specific antibodies and modulators are useful for treating a very wide range of diseases and conditions, e.g. wounds, ulcers, skin aging, obesity, diabetes, alopecia, inflammatory bowel disease, viral hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of the eye, etc.; also for maintaining organs before transplant and supporting culture of primary cells and tissues. Sequences AAG65647-67

CC represent amino acid sequences of some members of the FGF family

```
XX Sequence 209 AA;
SQ
Query Match 100.0%; Score 1113; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.2e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKPGVIQILGVKTSRFLCPDPCGALYGSLLHFDPEA 120
DB 61 LEIRDGTGGAADQSPESLLQKALKPGVIQILGVKTSRFLCPDPCGALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
```

RESULT 2

AA68417
ID AAB68417 standard; protein; 209 AA.

XX AC AAB68417;

XX DT 23-JUL-2001 (first entry)

XX DE Amino acid sequence of human fibroblast growth factor-21 (FGF-21).

XX KW Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation;
XX KW hepatic cell; cirrhosis; infertility; impotence; testicular cancer;
XX KW leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

XX OS Homo sapiens.

XX PN WO200136640-A2.

XX PD 25-MAY-2001.

XX PF 16-NOV-2000; 2000WO-US031745.

XX PR 18-NOV-1999; 99US-0166540P.

XX PR 11-MAY-2000; 2000US-0203633P.

XX PA (CHIR) CHIRON CORP.

XX PA (KYOU) UNIV KYOTO.

XX PI Itoh N, Kavanaugh WM;

XX DR WPI; 2001-343823/36.

XX DR N-PSDB; AAF85329.

XX PT New nucleic acid molecule useful for treating disease, e.g. infertility,
XX PT impotence, or testicular cancer.

XX PS Claim 14; Fig 5A-B; 61pp; English.

XX CC The present sequence represents a human fibroblast growth factor-21 (FGF-
XX CC 21). FGF proteins regulate growth and differentiation of a variety of
XX CC cell types. FGF-21 nucleic acids and polypeptides are useful for treating
XX CC diseases and disorders characterised by inadequate numbers of hepatic
XX CC cells, preferably cirrhosis of the liver. They may also be used in the
XX CC treatment of infertility, impotence, and testicular cancer, as well as
XX CC leukemia, lymphoma, autoimmune disease, or proliferative disorders of the
XX CC thymus

XX SQ sequence 209 AA;

```
Query Match 100.0%; Score 1113; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.2e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKPGVIQILGVKTSRFLCPDPCGALYGSLLHFDPEA 120
DB 61 LEIRDGTGGAADQSPESLLQKALKPGVIQILGVKTSRFLCPDPCGALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
```

RESULT 3

AAU79289

ID AAU79289 standard; protein; 209 AA.

XX AC AAU79289;

XX DT 13-AUG-2002 (first entry)

XX DE Human FGF-related protein.

XX KW Human; injury; burn; thrombosis; arteriosclerosis; pancreopathy;
XX KW hepatopathy; FGF-related protein.

XX OS Homo sapiens.

XX PN JP2002112772-A.

XX PD 16-APR-2002.

XX PF 04-SEP-2000; 2000JP-00271516.

XX PR 10-JUL-2000; 2000JP-00213385.

XX PR 03-AUG-2000; 2000JP-00240398.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX DR WPI; 2002-448752/48.

XX DR N-PSDB; ABK52425.

XX PT A protein and a partial peptide of the protein useful for treating
XX PT injuries, burns, thrombosis, arteriosclerosis, hepatopathy, pancreopathy,
XX PT and diabetes.

XX PS Claim 8; Fig 2; 44pp; Japanese.

XX CC The invention relates to a protein and the polynucleotide encoding it,
XX CC useful as drugs for injuries, burns, thrombosis, arteriosclerosis,
XX CC hepatopathy, pancreopathy and diabetes. This sequence represents a human
XX CC FGF-related protein of the invention

XX SQ Sequence 209 AA;

```
Query Match 100.0%; Score 1113; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.2e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60

DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRQRYLYTDDAQOTEAH 60

QY 61 LEIRDGTGGAADQSPESLLQKALKPGVIQILGVKTSRFLCPDPCGALYGSLLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGKTSRFLCQRPDGLGSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGLPALPEPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGLPALPEPGI 180
QY 181 LAPQPPDVGGSDPLSMVGFSGQSRSPSYAS 209
Db 181 LAPQPPDVGGSDPLSMVGFSGQSRSPSYAS 209

RESULT 4

ID AAE18826
XX AAE18826 standard; protein; 209 AA.

AC AAE18826;

DT 17-MAY-2002 (first entry)

DE Human FGF-21 protein.

XX Fibroblast growth factor; FGF-like protein; wound healing; bullosa;
KW epidermolysis; erosive gastritis; inflammatory bowel disease; ulcer;
KW oesophagitis; Crohn's disease; hyaline membrane disease; emphysema;
KW pulmonary fibrosis; hepatic cirrhosis; liver failure; angiogenesis;
KW multiple sclerosis; neurodegenerative disease; lung abnormality;
KW viral hepatitis; respiratory distress syndrome; tumour; skin aging;
KW gene therapy; vaccine; human.

XX Homo sapiens.

OS US2002001825-A1.

PN 03-JAN-2002.

XX 02-APR-2001; 2001US-00822485.

XX 31-MAR-2000; 2000US-00540118.

XX (ITOH/) ITOH N.

XX Itoh N;

XX WPI; 2002-187704/24.

XX Novel fibroblast growth factor-like polypeptide useful for treating,
PT ameliorating and/or preventing dermal wounds, gastric ulcer, Crohn's
PT disease and pulmonary inflammation.

XX Disclosure; Fig 3; 63pp; English.

XX The invention relates to fibroblast growth factor (FGF)-like polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating, preventing or ameliorating a medical
CC condition. They are useful for treating dermal wounds, epidermolysis,
CC bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive
CC gastritis, oesophagitis, oesophageal reflux disease, inflammatory bowel
CC disease, Crohn's disease, radiation- or chemotherapy-induced gut
CC toxicity, hyaline membrane disease, necrosis of the respiratory
CC epithelium, emphysema, pulmonary inflammation, pulmonary fibrosis,
CC hepatic cirrhosis, toxic insults to the liver, fulminant liver failure,
CC viral hepatitis, mucositis, multiple sclerosis and other
CC neurodegenerative diseases, infantile respiratory distress syndrome,
CC bronchopulmonary dysplasia, acute respiratory distress syndrome or other
CC lung abnormalities, tumours of the eye or the other tissues and organs.
CC FGF-like polypeptides are useful stimulating angiogenesis, promoting
CC wound healing, modulating differentiation of neuronal cells, adipocytes
CC and skeletal muscle cells, preventing or ameliorate skin aging,
CC preventing hair loss, stimulating the growth and differentiation of
CC haematopoietic cells and bone marrow cells and maintaining organs before
CC transplantation and for supporting cultures of primary cells and tissues.
CC Sequences of the invention are also used in gene therapy and as vaccines.

CC The present sequence is human FGF-21 protein which is a member of the FGF
CC family
XX
SQ Sequence 209 AA;

Query Match 100.0%; Score 1113; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.2e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLGALLGACQAHPIPDSSPLQFGGVQRVLYTDDAQTEAH 60

Db 1 MDSDETFEHSGLWVSVLGALLGACQAHPIPDSSPLQFGGVQRVLYTDDAQTEAH 60

QY 61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGKTSRFLCQRPDGLGSLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALKPGVIQILGKTSRFLCQRPDGLGSLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGLPALPEPGI 180

Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGLPALPEPGI 180

QY 181 LAPQPPDVGGSDPLSMVGFSGQSRSPSYAS 209

Db 181 LAPQPPDVGGSDPLSMVGFSGQSRSPSYAS 209

RESULT 5

ADM94766

ID ADM94766 standard; protein; 209 AA.

XX ADM94766;

DT 17-JUN-2004 (first entry)

XX Human fibroblast growth factor (FGF) protein, FGF-21.

XX human; fibroblast growth factor; FGF; epidermolysis bullosa;
KW chemotherapy-induced alopecia; male baldness; gastric ulcer;
KW duodenal ulcer; stomach erosion; oesophagus erosion;
KW inflammatory bowel disease; Crohn's disease; hyaline membrane disease;
KW smoke inhalation; emphysema; hepatic cirrhosis;
KW thymic epithelial atrophy.

XX Homo sapiens.

XX US2003170822-A1.

XX 11-SEP-2003.

XX 25-FEB-2003; 2003US-00374207.

XX 31-MAR-2000; 2000US-00540118.

XX 02-APR-2001; 2001US-00822485.

XX (ITOH/) ITOH N.

XX Itoh N;

XX WPI; 2004-119152/12.

XX New nucleic acid encoding a fibroblast growth factor-like polypeptide is
PT useful to diagnose, treat, ameliorate or prevent associated diseases
PT including epidermolysis bullosa, cirrhosis, hair loss and gastric and
PT duodenal ulcers.

XX Disclosure; SEQ ID NO 24; 63pp; English.

XX The invention relates to an isolated nucleic acid comprising a sequence
CC encoding a human fibroblast growth factor (FGF)-like polypeptide. The
CC invention is useful to diagnose, prevent, treat or ameliorate diseases or
CC conditions associated with FGF-like polypeptide including epidermolysis
CC bullosa, chemotherapy-induced alopecia, male baldness, gastric and
CC duodenal ulcers, erosions of the stomach and oesophagus, inflammatory

CC bowel disease such as Crohn's disease, hyaline membrane disease of
CC premature infants, smoke inhalation, emphysema, hepatic cirrhosis and
CC thymic epithelial atrophy. The nucleic acids may also be used to map
CC locations of FGF-like gene and related genes on chromosomes. The present
XX sequence represents a human FGF protein.
SQ Sequence 209 AA;

Query Match 100.0%; Score 1113; DB 8; Length 209;
Best Local Similarity 100.0%; Pred. No. 6.2e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTDDAQOTEAH 60

Qy 61 LEIRDGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
Db 61 LEIRDGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120

Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

Qy 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 6
ADL57117
ID ADL57117 standard; protein; 209 AA.
AC ADL57117;
DT 03-JUN-2004 (first entry)
DE Human NOV6e protein SEQ ID NO:62.
XX human; antidiabetic; anorectic; cardiant; hypotensive;
XX antihypertensive; anorectic; virucide; antibacterial; fungicide;
XX protocoarctid; neuroprotective; antiparkinsonian;
XX anticonvulsant; osteoparctid; antihypertensive; antidiabetic;
XX dermatological; antidiabetic; antiparkinsonian; antidiabetic;
XX fibroblast growth factor receptor 4; FGFR4;
XX complement factor I precursor; matrix metalloproteinase-15 precursor;
XX MDC3; T-lymphocyte surface antigen Ly-9 precursor;
XX fibroblast growth factor-21; FGF-21;
XX alpha-2 macroglobulin-like polypeptide variant;
XX antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
XX transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX Homo sapiens.
OS
XX
XX WO2004022723-A2.
XX
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-US028141.
XX
XX 09-SEP-2002; 2002US-0409145P.
XX 10-SEP-2002; 2002US-0409544P.
XX 12-SEP-2002; 2002US-0410320P.
XX 16-SEP-2002; 2002US-0411060P.
XX 23-SEP-2002; 2002US-0412766P.
XX 23-SEP-2002; 2002US-0412825P.
XX 24-SEP-2002; 2002US-0412767P.
XX 25-SEP-2002; 2002US-0413342P.
XX 30-SEP-2002; 2002US-0414832P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;

XX WPI: 2004-315567/29.
DR N-PSDB; ADL57116.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX Claim 1; SEQ ID NO 62; 214pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiant, hypotensive, antihypertensive, anorectic,
CC virucide, antibacterial, fungicide, protocoarctid, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteoparctid, and
CC antihypertensive activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
XX
SQ Sequence 209 AA;

Query Match 99.6%; Score 1109; DB 8; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.4e-91;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTDDAQOTEAH 60

Qy 61 LEIRDGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
Db 61 LEIRDGTGGAADQSPESLLQKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120

Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

Qy 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209


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RESULT 7
ADL57121
ID ADL57121 standard; protein; 209 AA.
XX
AC ADL57121;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOV6g protein SEQ ID NO:66.
XX
KW human; antidiabetic; anorectic; cardiatic; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipaeamic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor 1 precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoprotease 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX
OS Homo sapiens.
XX
XX WO2004022723-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-US028141.
XX
PR 09-SEP-2003; 2002US-0409145P.
PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
XX
DR WPI; 2004-315567/29.
XX
DR N-PSDB; ADL57120.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 66; 214pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiatic, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipaeamic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders

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CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor 1 precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoprotease 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
XX
SQ Sequence 209 AA;
XX
Query Match 99.6%; Score 1109; DB 8; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.4e-91;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLFLQFGQVQRVLYTDDAQTEAH 60
DB 1 MDSDETFEHSGLWVSLAGLLGACQAHPIPDSSPLFLQFGQVQRVLYTDDAQTEAH 60
QY 61 LEIREDTGVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQPDGALYGLSHFDPEA 120
DB 61 LEIREDTGVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQPDGALYGLSHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
QY 181 LAPQPDVGVSSDPLSMVGFSGRSPSYAS 209
DB 181 LAPQPDVGVSSDPLSMVGFSGRSPSYAS 209
RESULT 8
ADL57125
ID ADL57125 standard; protein; 209 AA.
XX
AC ADL57125;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOV6i protein SEQ ID NO:70.
XX
KW human; antidiabetic; anorectic; cardiatic; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipaeamic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor 1 precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoprotease 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX
OS Homo sapiens.
XX
XX WO2004022723-A2.
XX
PN
XX

```


CC The invention relates to a novel isolated polypeptide (NOVX) comprising a
 CC mature form of any of the 37 amino acid sequences fully defined in the
 CC specification. A polypeptide of the invention has antidiabetic,
 CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
 CC virucide, antibacterial, fungicide, protozoacide, neurotropic,
 CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
 CC antiarthritic, antiinflammatory, dermatological, antisthmatic, and
 CC antilipaemic activity. A polynucleotide of the invention may have a use
 CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
 CC are useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOVX-associated disorder.
 CC The nucleic acid molecules, polypeptides and antibodies are useful for
 CC treating, preventing or diagnosing diseases such as metabolic disorders,
 CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
 CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
 CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
 CC disease, Parkinson's disease, epilepsy, immune disorders
 CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
 CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridisation probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
 CC polypeptides of the invention show homology to certain known human
 CC proteins: NOV1a-11 show homology to fibroblast growth factor receptor 4
 CC (FGFR4); NOV2a shows homology to complement factor 1 precursor; NOV3a
 CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
 CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
 CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
 CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
 CC polypeptide variant; NOV8a-8g show homology to antileukoprotease 1
 CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
 CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
 CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
 CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
 CC of the invention.
 CC
 CC Sequence 209 AA;

Query Match 99.5%; Score 1107; DB 8; Length 209;
 Best Local Similarity 99.5%; Pred. No. 2.1e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDSDETPHESGLWVSVLGALLGACQAHPIPDSSPLQLQFGQVQRVLYTDDAQOTRAH 60
 Db 1 MDSDEIGFHSGLWVSVLGALLGACQAHPIPDSSPLQLQFGQVQRVLYTDDAQOTRAH 60
 QY 61 LEIRDGTGGAADQSPESLLQLKALFQVIQILGVKTSRFLCQPDGALYGSLLHFDPEA 120
 Db 61 LEIRDGTGGAADQSPESLLQLKALFQVIQILGVKTSRFLCQPDGALYGSLLHFDPEA 120
 QY 121 CSFRELLEDGNYVQSEAHGLPLHLPGNKSHPRDAPRGPARFLPLGLPPALPEPGGI 180
 Db 121 CSFRELLEDGNYVQSEAHGLPLHLPGNKSHPRDAPRGPARFLPLGLPPALPEPGGI 180
 QY 181 LAPQPPDVGSSDPLSMVGSPQGRSPSYAS 209
 Db 181 LAPQPPDVGSSDPLSMVGSPQGRSPSYAS 209

RESULT 10
 ADL57127

ID ADL57127 standard; protein; 209 AA.

AC ADL57127;

XX ADL57127;

DT 03-JUN-2004 (first entry)

XX Human NOV6j protein SEQ ID NO:72.

XX

KW human; antidiabetic; anorectic; cardiant; hypotensive;
 KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
 KW protozoacide; neurotropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
 KW dermatological; antisthmatic; antilipaemic; gene therapy;
 KW fibroblast growth factor receptor 4; FGFR4;
 KW complement factor 1 precursor; matrix metalloproteinase-15 precursor;
 KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
 KW fibroblast growth factor-21; FGF-21;
 KW alpha-2 macroglobulin-like polypeptide variant;
 KW antileukoprotease 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
 KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004022723-A2.
 XX
 XX 18-MAR-2004.
 XX
 XX 09-SEP-2003; 2003WO-US028141.
 PF
 XX 09-SEP-2002; 2002US-0409145P.
 PR 10-SEP-2002; 2002US-0409544P.
 PR 12-SEP-2002; 2002US-0410320P.
 PR 16-SEP-2002; 2002US-0411060P.
 PR 23-SEP-2002; 2002US-0412766P.
 PR 23-SEP-2002; 2002US-0412825P.
 PR 24-SEP-2002; 2002US-0412767P.
 PR 25-SEP-2002; 2002US-0413342P.
 PR 30-SEP-2002; 2002US-0414832P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
 PI
 XX WPI, 2004-315567/29.
 XX N-PsDB; ADL57126.
 DR
 XX
 PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 PT
 XX Claim 1; SEQ ID NO 72; 214pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
 CC mature form of any of the 37 amino acid sequences fully defined in the
 CC specification. A polypeptide of the invention has antidiabetic,
 CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
 CC virucide, antibacterial, fungicide, protozoacide, neurotropic,
 CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, and
 CC antiarthritic, antiinflammatory, dermatological, antisthmatic, and
 CC antilipaemic activity. A polynucleotide of the invention may have a use
 CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
 CC are useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOVX-associated disorder.
 CC The nucleic acid molecules, polypeptides and antibodies are useful for
 CC treating, preventing or diagnosing diseases such as metabolic disorders,
 CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
 CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
 CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
 CC disease, Parkinson's disease, epilepsy, immune disorders
 CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
 CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridisation probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
 CC polypeptides of the invention show homology to certain known human
 CC proteins: NOV1a-11 show homology to fibroblast growth factor receptor 4

CC (FGR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoprotease 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC of the invention.
XX
SQ Sequence 209 AA;

Query Match 99.5%; Score 1107; DB 8; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.1e-91;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSDETGFHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTTDDAQOTEAH 60
DB 1 MDSDETGFHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTTDDAQOTEAH 60
QY 61 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGSLSHFDEA 120
DB 61 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGSLSHFDEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPKGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPKGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGGSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGGSDPLSMVGPQGRSPSYAS 209

RESULT 11

ADL57129

ID ADL57129 standard; protein; 209 AA.

AC ADL57129;

XX 03-JUN-2004 (first entry)

XX Human NOV6k protein SEQ ID NO:74.

XX human; antidiabetic; anorectic; cardiac; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipase; gene therapy;
KW fibroblast growth factor receptor 4; FGR4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoprotease 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.

XX Homo sapiens.

OS

XX

PN WO2004022723-A2.

XX

XX

PD 18-MAR-2004.

XX

XX

XX

XX

XX

XX

XX

XX

PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX (CURA-) CURAGEN CORP.

XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
PI WPI; 2004-315567/29.
XX N-PSDB; ADL57128.

DR New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX Claim 1; SEQ ID NO 74; 214pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
FS mature form of any of the 37 amino acid sequences fully defined in the
XX specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiac, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, nootropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipase activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoprotease 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.

XX Sequence 209 AA;

Query Match 99.5%; Score 1107; DB 8; Length 209;

Best Local Similarity 99.5%; Pred. No. 2.1e-91;

Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETGFHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTTDDAQOTEAH 60
DB 1 MDSDETGFHSGLWVSVLAGLLGACQAHPTDSSPLLQFGQVQRVLYTTDDAQOTEAH 60

QY 61 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGSLSHFDEA 120
DB 61 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGSLSHFDEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPKGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPKGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180

Db 121 CSFRELLEDGYNVQSEAHGLPLHLPGNKSPhRDPAFGPARFLPLQCPALPEPCCI 180
 QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 12
 AAB82351
 ID AAB82351 standard; protein; 209 AA.
 AC AAB82351;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Human JAFFA protein.
 XX
 KW JAFFA; human; fibroblast growth factor; diagnosis; therapy; cancer;
 KW autoimmune disease; cytostatic; immunosuppressive; neuroprotective.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..28
 FT /label= Signal_peptide
 FT 6..9
 FT Modified-site /note= "predicted casein kinase II phosphorylation site"
 FT 12..17
 FT Modified-site /note= "N-myristoylation"
 FT 20..25
 FT Modified-site /note= "N-myristoylation"
 FT 29..209
 FT Protein /label= Mature_protein
 FT 60..140
 FT Domain /note= "fibroblast growth factor domain"
 FT 67..72
 FT Modified-site /note= "N-myristoylation"
 FT 95..100
 FT Modified-site /note= "N-myristoylation"
 FT 98..100
 FT Modified-site /note= "protein kinase C predicted phosphorylation site"
 FT 108..113
 FT Modified-site /note= "N-myristoylation"
 FT 122..125
 FT Modified-site /note= "predicted casein kinase II phosphorylation site"
 FT 122..124
 FT Modified-site /note= "protein kinase C predicted phosphorylation site"
 XX
 PN WO200138357-A2.

31-MAY-2001.
 XX
 PD 22-NOV-2000; 2000WO-US032181.
 XX
 PF 22-NOV-1999; 99US-00444165.
 XX
 PR (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Khodadoust MM;
 XX
 XX WPI; 2001-355881/37.
 DR N-PSDB; AAF90326, AAF90327.
 XX
 XX Isolated JAFFA nucleic acid molecules which encode novel fibroblast
 PT growth factor family members (JAFFA) are useful for developing novel
 PT diagnostic and therapeutic agents for JAFFA-associated disorders such as
 PT cancers.
 XX
 XX Claim 2; Fig 1; 137pp; English.
 PS
 PS The present sequence is that of human JAFFA, a novel member of the
 CC fibroblast growth factor family. Analysis of rare sequences in the
 CC Millennium database led to the identification of an expressed sequence

CC tag from a human prostate tumour library which coded for a novel
 CC hypothetical signal peptide. Further analysis led to the identification
 CC of JAFFA. The invention provides JAFFA polypeptides, polynucleotides and
 CC anti-JAFFA antibodies. It also provides antisense nucleic acid molecules,
 CC recombinant expression vectors, host cells and transgenic animals. JAFFA
 CC proteins may be useful for developing novel diagnostic and therapeutic
 CC agents for JAFFA-associated disorders such as cancers and other disorders
 CC which demonstrate ABO(H) blood group disorders and for controlling
 CC cellular proliferative and/or differentiative disorders. The JAFFA
 CC nucleic acid and protein may be used to treat and/or diagnose a variety
 CC of immune disorders such as autoimmune disease and multiple sclerosis.
 CC The proteins may also be used to screen for naturally occurring JAFFA
 CC substrates, to screen for drugs or compounds which modulate JAFFA
 CC activity, and to raise anti-JAFFA antibodies, which can be used to detect
 CC and isolate JAFFA proteins, regulate the bioavailability of JAFFA
 CC proteins and modulate JAFFA activity
 XX
 SQ Sequence 209 AA;

Query Match 99.4%; Score 1106; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. NO. 2.6e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLMVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQTAAH 60
 Db 1 MDSDETFEHSGLMVSVLAGLLGACQAHPIPDSSPLQFGQVQRVLYTDDAQTAAH 60
 QY 61 LEIRDGTGVCAGADQSPESLLQLKALPGVITQLGVKTSRFLCQRPDGLYGLHFDPEA 120
 Db 61 LEIRDGTGVCAGADQSPESLLQLKALPGVITQLGVKTSRFLCQRPDGLYGLHFDPEA 120
 QY 121 CSFRELLLEDGYNVQSEAHGLPLHLPGNKSPhRDPAFGPARFLPLQCPALPEPCCI 180
 Db 121 CSFRELLLEDGYNVQSEAHGLPLHLPGNKSPhRDPAFGPARFLPLQCPALPEPCCI 180
 QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 13
 AAU00957
 ID AAU00957 standard; protein; 209 AA.
 AC AAU00957;
 XX
 DT 24-MAY-2001 (first entry)
 XX
 DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide.

XX Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
 KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
 KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
 KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;
 KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
 KW multiple sclerosis; short stature; delayed maturation; excessive growth;
 KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
 KW androgen target organ abnormality; respiratory distress syndrome; stroke;
 KW cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness;
 KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
 KW decreased stamina; decreased cardiac function; immune system dysfunction;
 KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;
 KW senile dementia; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT /note= "Signal peptide"
 FT 29..209
 FT Protein /note= "Mature human FGF-like protein"
 XX
 PN WO200118172-A2.

```
XX PD 15-MAR-2001.
XX PF 05-SEP-2000; 2000WO-US024373.
XX PR 07-SEP-1999; 99US-00391861.
XX PR 23-AUG-2000; 2000US-00644052.
XX PA (AMGE-) AMGEN INC.
XX PI Thomason AR, Liu B;
XX PI WPI; 2001-226743/23.
XX DR N-FSDB; AAS00779.
XX PT Novel isolated fibroblast growth factor-like polypeptide useful for
XX PT treating, preventing or ameliorating cirrhosis, inflammatory bowel
XX PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
XX PT osteoporosis.
XX PS Claim 13; Fig 2; 138pp; English.
XX CC The sequence represents a fibroblast growth factor-like (FGF-like)
XX CC polypeptide. FGF-like protein and its associated nucleic acid play a role
XX CC in modulating body growth, maturation or life-span. They are also useful
XX CC for treating, preventing or ameliorating disorders such as cirrhosis,
XX CC inflammatory bowel disease, mucositis, Crohn's disease, diabetes,
XX CC obesity, gastrointestinal abnormalities, neurodegenerative diseases,
XX CC damage to renal tubules as a result of acute tubular necrosis,
XX CC haematopoietic cell reconstitution following chemotherapy, wasting
XX CC syndromes (e.g., cancer associated cachexia), damage to the corneal
XX CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
XX CC stature, delayed maturation, excessive growth (e.g. acromegaly),
XX CC premature maturation, alopecia, abnormalities of androgen target organs,
XX CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
XX CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,
XX CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
XX CC baldness, wrinkles, increased fatigue, decreased stamina, decreased
XX CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,
XX CC senile dementia, Alzheimer's disease, and decreased cognitive function
XX SQ
XX Sequence 209 AA;
Query Match 99.4%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.6e-91;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
DB 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
QY 121 CSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLPGLPAPPEPGI 180
DB 121 CSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLPGLPAPPEPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
RESULT 14
ID AAB83951
XX AAB83951 standard; protein; 209 AA.
XX AC AAB83951;
XX DT 06-AUG-2001 (first entry)
XX DE Amino acid sequence of a human sbgFGF-19a polypeptide.
```

```
XX KW Human; sbgFGF-19a; fibroblast growth factor; stroke; cancer; psoriasis;
XX KW traumatic brain injury; cerebral ischemia; atherosclerosis;
XX KW rheumatoid arthritis; cirrhosis; sarcoidosis; wound repair;
XX KW idiopathic pulmonary fibrosis; tumour development;
XX KW vaccine developmental disorder; skeletal disorder; acrocephaly.
XX OS Homo sapiens.
XX PN WO200132678-A1.
XX PD 10-MAY-2001.
XX PF 03-NOV-2000; 2000WO-US030478.
XX PR 05-NOV-1999; 99US-00434358.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Agarwal P, Barone F, Feild JA, Kabnick KS, Mcquaney MS;
XX PI WPI; 2001-316413/33.
XX DR N-FSDB; AAF89921.
XX PT Novel sbgFGF-19a polypeptide, a member of fibroblast growth factor family
XX PT and polynucleotides encoding them useful for diagnosing, treating stroke,
XX PT psoriasis, cancer, atherosclerosis, rheumatoid arthritis and cirrhosis.
XX PS Claim 1; Page 23; 31pp; English.
XX CC The present sequence represents a human sbgFGF-19a polypeptide. The
XX CC polypeptide is a member of fibroblast growth factor family of
XX CC polypeptides. The polynucleotides and polypeptides are useful in the
XX CC treatment of diseases such as stroke, traumatic brain injury, cerebral
XX CC ischemia, cancer, atherosclerosis, rheumatoid arthritis, cirrhosis,
XX CC psoriasis, sarcoidosis, idiopathic pulmonary fibrosis, tumour
XX CC development, developmental disorders, skeletal disorders, wound repair,
XX CC and acrocephaly. They are also useful as vaccines for inducing an
XX CC immunological response in a mammal
XX SQ
XX Sequence 209 AA;
Query Match 99.4%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.6e-91;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOTEAH 60
QY 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
DB 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFLCQRPDQALYGSLLHFDPEA 120
QY 121 CSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLPGLPAPPEPGI 180
DB 121 CSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLPGLPAPPEPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
RESULT 15
ADL57111
ID ADL57111 standard; protein; 209 AA.
XX AC ADL57111;
XX DT 03-JUN-2004 (first entry)
XX DE Human NOV6b protein SEQ ID NO:56.
XX
```


KW human; antidiabetic; anorectic; cardiant; hypotensive;
KW antihypertensive; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX Homo sapiens.
OS
XX
XX WO2004022723-A2.
XX
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-US028141.
XX
XX 09-SEP-2002; 2002US-0409145P.
PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
XX
XX WPI: 2004-315567/29.
XX N-PSDB; ADL57110.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
XX asthma, or infections.
XX
XX Claim 1; SEQ ID NO 56; 214pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
XX mature form of any of the 37 amino acid sequences fully defined in the
XX specification. A polypeptide of the invention has antidiabetic,
XX anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
XX virucide, antibacterial, fungicide, protozoacide, neurotropic,
XX neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
XX antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
XX antilipemic activity. A polynucleotide of the invention may have a use
XX in gene therapy. The polypeptides, nucleic acid molecules and antibodies
XX are useful in the manufacture of a medicament for treating a syndrome
XX associated with a human disease, preferably a NOVX-associated disorder.
XX The nucleic acid molecules, polypeptides and antibodies are useful for
XX treating, preventing or diagnosing diseases such as metabolic disorders,
XX diabetes, obesity, infectious diseases (viral, bacterial, fungal,
XX helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
XX (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
XX disease, Parkinson's disease, epilepsy, immune disorders
XX (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
XX asthma, and various dyslipidaemias. The nucleic acids and polypeptides
XX may also be used as targets for the identification of small molecules
XX that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
XX proliferation, haematopoiesis, wound healing and angiogenesis, in gene
XX therapy. In generation of antibodies that bind immunospecifically to NOVX
XX substances for use in therapeutic or diagnostic methods. The nucleic
XX acids are further used as hybridisation probes, in chromosome mapping,
XX tissue typing, preventive medicine, and pharmacogenomics. The NOVX
XX polypeptides of the invention show homology to certain known human
XX proteins: NOV1a-it show homology to fibroblast growth factor receptor 4

CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
XX
XX SQ Sequence 209 AA;

Query Match 99.4%; Score 1106; DB 8; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.6e-91;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MDSDTGFEHSLWVSLAGLLGACQAHPIPDSSPLQFGQVQRVLYTTDDAQOQTEAH 60
QY 61 LEIREDTGVGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGLHFDPEA 120
DB 61 LEIREDTGVGGAADQSPESLLQKALKEGVIQILGVKTSRFLCORPDGALYGLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGCLPPALPEPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGCLPPALPEPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

Search completed: July 8, 2005, 22:13:07
Job time : 277.442 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:22:45 ; Search time 163 Seconds
(without alignments)
495,907 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 209

Sequence: 1 MDSDTGFHSLVWVLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table:  Gapop-60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	209	4	AAG65667 Human fib
2	209	100.0	209	4	AAB68417 Amino aci
3	209	100.0	209	5	AAU79289 Human FGF
4	209	100.0	209	5	AAE18826 Human FGF
5	209	100.0	209	8	ADM94766 Human fib
6	203	97.1	209	8	ADL57123 Human NOV
7	203	97.1	209	8	ADL57125 Human NOV
8	192	91.9	209	8	ADL57121 Human NOV
9	188	90.0	208	4	AAE05078 Human fib
10	188	90.0	208	5	AAU83630 Human PRO
11	188	90.0	208	5	ABG32358 Human fib
12	188	90.0	208	5	ABG17601 Human ext
13	188	90.0	208	6	ABU80777 Human PRO
14	188	90.0	208	6	ABO33743 Novel hum
15	188	90.0	208	6	ABU82086 Novel hum
16	188	90.0	208	6	ABP96156 Human fib
17	188	90.0	208	6	ABJ72366 Human PRO
18	188	90.0	208	6	ABJ72394 Human PRO
19	188	90.0	208	6	ABO34289 Human sec
20	188	90.0	208	7	ADA37038 Human fib
21	188	90.0	208	7	ABJ72096 Human mem
22	188	90.0	208	7	ADB83568 Novel hum
23	188	90.0	208	7	ADB80674 Novel hum
24	188	90.0	208	7	ADB73215 Novel hum
25	188	90.0	208	7	ADB78297 Novel hum

26	188	90.0	208	7	ADB84945 Human PRO
27	188	90.0	208	7	ADB78051 Novel hum
28	188	90.0	208	7	ADB87117 Human PRO
29	188	90.0	208	7	ADB84699 Human PRO
30	188	90.0	208	7	ADB83814 Novel hum
31	188	90.0	208	7	ADB72969 Novel hum
32	188	90.0	208	7	ADC36807 Human PRO
33	188	90.0	208	7	ADC21797 Human PRO
34	188	90.0	208	7	ADC49828 Novel hum
35	188	90.0	208	7	ADC49027 Novel hum
36	188	90.0	208	7	ADC49544 Novel hum
37	188	90.0	208	7	ADC47405 Novel hum
38	188	90.0	208	7	ADC47150 Novel hum
39	188	90.0	208	7	ADC78025 Novel hum
40	188	90.0	208	7	ADD06260 Novel hum
41	188	90.0	208	7	ADC77779 Novel hum
42	188	90.0	208	7	ADD50742 Novel hum
43	188	90.0	208	7	ADD50988 Novel hum
44	188	90.0	208	7	ADD50469 Human PRO
45	188	90.0	208	7	ADD50223 Human PRO

ALIGNMENTS

RESULT 1

AAAG65667
ID AAG65667 standard; protein; 209 AA.

XX AC AAG65667;

XX DT 07-JAN-2002 (first entry)

XX DE Human fibroblast growth factor (FGF)-21..

XX KW Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic; fat deposition; vulnery; antitumor; dermatological; anorectic; antidiabetic; antiinflammatory; cytostatic; hepatic; virucide; neuroprotectant; pulmonary; gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN WO200172957-A2.

XX PD 04-OCT-2001.

XX PF 02-APR-2001; 2001WO-IB000664.

XX PR 31-MAR-2000; 2000US-00540118.

XX PA (ITOH/) ITOH N.

XX PI Itoh N;

XX DR WPI; 2001-611623/70.

XX PT New human nucleic acid encoding fibroblast growth factor-like peptide, useful for treatment and diagnosis of e.g. wounds and inflammatory bowel disease.

XX PS Disclosure; Fig 3; 172pp; English.

XX CC The invention provides human nucleic acids encoding fibroblast growth factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by standard recombinant methodology and are mitogenic for a wide range of cells, inducing differentiation and proliferation, and inhibiting deposition of fat. The FGF-like polypeptides, polynucleotides and specific antibodies and modulators are useful for treating a very wide range of diseases and conditions, e.g. wounds, ulcers, skin aging, obesity, diabetes, alopecia, inflammatory bowel disease, viral hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of the eye, etc., also for maintaining organs before transplant and supporting culture of primary cells and tissues. Sequences AAG65647-67

CC represent amino acid sequences of some members of the FGF family
XX Sequence 209 AA;

Query Match 100.0%; Score 209; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 1.1e-190;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
QY 61 LEIREDTGTVGGAAADQSPESLLQKALKPGVIQILGVTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIREDTGTVGGAAADQSPESLLQKALKPGVIQILGVTSRFLCQRPDGCALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 2

ID AAB68417 standard; protein; 209 AA.

AC AAB68417;

DT 23-JUL-2001 (first entry)

XX Amino acid sequence of human fibroblast growth factor-21 (FGF-21).

XX Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation;
KW hepatic cell; cirrhosis; infertility; impotence; testicular cancer;
KW leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

XX Homo sapiens.

XX WO200136640-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031745.

XX 18-NOV-1999; 99US-0166540P.

XX 11-MAY-2000; 2000US-0203633P.

XX (CHTR) CHIRON CORP.

XX (KYOU) UNIV KYOTO.

XX Itoh N, Kavanaugh WM;

XX WPI; 2001-343823/36.

XX N-PSDB; AAF85329.

XX New nucleic acid molecule useful for treating disease, e.g. infertility,
PT impotence, or testicular cancer.

XX Claim 14; Fig 5A-B; 61pp; English.

XX The present sequence represents a human fibroblast growth factor-21 (FGF-
CC 21). FGF proteins regulate growth and differentiation of a variety of
CC cell types. FGF-21 nucleic acids and polypeptides are useful for treating
CC diseases and disorders characterised by inadequate numbers of hepatic
CC cells, preferably cirrhosis of the liver. They may also be used in the
CC treatment of infertility, impotence, and testicular cancer, as well as
CC leukemia, lymphoma, autoimmune disease, or proliferative disorders of the
CC thymus

XX Sequence 209 AA;

Query Match 100.0%; Score 209; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 1.1e-190;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGTVGGAAADQSPESLLQKALKPGVIQILGVTSRFLCQRPDGCALYGSLLHFDPEA 120

DB 61 LEIREDTGTVGGAAADQSPESLLQKALKPGVIQILGVTSRFLCQRPDGCALYGSLLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGI 180

DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 3

AAU79289

ID AAU79289 standard; protein; 209 AA.

XX AAU79289;

XX 13-AUG-2002 (first entry)

XX Human FGF-related protein.

XX Human; injury; burn; thrombosis; arteriosclerosis; pancreopathy;
KW hepatopathy; FGF-related protein.

XX Homo sapiens.

XX JP2002112772-A.

XX 16-APR-2002.

XX 04-SEP-2000; 2000JP-00271516.

XX 10-JUL-2000; 2000JP-00213385.

XX 03-AUG-2000; 2000JP-00240398.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2002-448752/48.

XX N-PSDB; ABK52425.

XX A protein and a partial peptide of the protein useful for treating
PT injuries, burns, thrombosis, arteriosclerosis, hepatopathy, pancreopathy,
PT and diabetes.

XX Claim 8; Fig 2; 44pp; Japanese.

XX The invention relates to a protein and the polynucleotide encoding it,
CC useful as drugs for injuries, burns, thrombosis, arteriosclerosis,
CC hepatopathy, pancreopathy and diabetes. This sequence represents a human
CC FGF-related protein of the invention

XX Sequence 209 AA;

Query Match 100.0%; Score 209; DB 5; Length 209;

Best Local Similarity 100.0%; Pred. No. 1.1e-190;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60

QY 61 LEIREDTGTVGGAAADQSPESLLQKALKPGVIQILGVTSRFLCQRPDGCALYGSLLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALPGVVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 4

ID AAE18826 standard; protein; 209 AA.

AC AAE18826;

DT 17-MAY-2002 (first entry)

DE Human FGF-21 protein.

XX Fibroblast growth factor; FGF-like protein; wound healing; bullosa;
KW epidermolysis; erosive gastritis; inflammatory bowel disease; ulcer;
KW oesophagitis; Crohn's disease; hyaline membrane disease; emphysema;
KW pulmonary fibrosis; hepatic cirrhosis; liver failure; angiogenesis;
KW multiple sclerosis; neurodegenerative disease; lung abnormality;
KW viral hepatitis; respiratory distress syndrome; tumour; skin aging;
KW gene therapy; vaccine; human.

XX Homo sapiens.

OS US2002001825-A1.

PN 03-JAN-2002.

PD 02-APR-2001; 2001US-00822485.

PF 31-MAR-2000; 2000US-00540118.

PR (ITOH/) ITOH N.

PI Itoh N;

PS WPI; 2002-187704/24.

XX Novel fibroblast growth factor-like polypeptide useful for treating,
PT ameliorating and/or preventing dermal wounds, gastric ulcer, Crohn's
PT disease and pulmonary inflammation.

XX Disclosure; Fig 3; 63pp; English.

XX The invention relates to fibroblast growth factor (FGF)-like polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating, preventing or ameliorating a medical
CC condition. They are useful for treating dermal wounds, epidermolysis,
CC bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive
CC gastritis, oesophagitis, oesophageal reflux disease, inflammatory bowel
CC disease, Crohn's disease, radiation- or chemotherapy-induced gut
CC toxicity, hyaline membrane disease, necrosis of the respiratory
CC epithelium, emphysema, pulmonary inflammation, pulmonary fibrosis,
CC hepatic cirrhosis, toxic insults to the liver, fulminant liver failure,
CC viral hepatitis, mucositis, multiple sclerosis and other
CC neurodegenerative diseases, infantile respiratory distress syndrome,
CC bronchopulmonary dysplasia, acute respiratory distress syndrome or other
CC lung abnormalities, tumours of the eye or the other tissues and organs.
CC FGF-like polypeptides are useful stimulating angiogenesis, promoting
CC wound healing, modulating differentiation of neuronal cells, adipocytes
CC and skeletal muscle cells, preventing or ameliorate skin aging.
CC preventing hair loss, stimulating the growth and differentiation of
CC haematopoietic cells and bone marrow cells and maintaining organs before
CC transplantation and for supporting cultures of primary cells and tissues.
CC Sequences of the invention are also used in gene therapy and as vaccines.

CC The present sequence is human FGF-21 protein which is a member of the FGF
CC family

SQ Sequence 209 AA;

Query Match 100.0%; Score 209; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETGFHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQTEAH 60

Db 1 MDSDETGFHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQTEAH 60

QY 61 LEIREDTGTVGGAADQSPESLLQKALPGVVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120

Db 61 LEIREDTGTVGGAADQSPESLLQKALPGVVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPALPEPPGI 180

Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPA PRGPAPRFLPLGLPPALPEPPGI 180

QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

Db 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 5

ID ADM94766 standard; protein; 209 AA.

AC ADM94766;

DT 17-JUN-2004 (first entry)

DE Human fibroblast growth factor (FGF) protein, FGF-21.

XX human; fibroblast growth factor; FGF; epidermolysis bullosa;
KW chemotherapy-induced alopecia; male baldness; gastric ulcer;
KW duodenal ulcer; stomach erosion; oesophagus erosion;
KW inflammatory bowel disease; Crohn's disease; hyaline membrane disease;
KW smoke inhalation; emphysema; hepatic cirrhosis;
KW thymic epithelial atrophy.

XX Homo sapiens.

PN US2003170822-A1.

XX 11-SEP-2003.

XX 25-FEB-2003; 2003US-00374207.

XX 31-MAR-2000; 2000US-00540118.

PR 02-APR-2001; 2001US-00822485.

PA (ITOH/) ITOH N.

PI Itoh N;

PS WPI; 2004-119152/12.

XX New nucleic acid encoding a fibroblast growth factor-like polypeptide is
PT useful to diagnose, treat, ameliorate or prevent associated diseases
PT including epidermolysis bullosa, cirrhosis, hair loss and gastric and
PT duodenal ulcers.

XX Disclosure; SEQ ID NO 24; 63pp; English.

XX The invention relates to an isolated nucleic acid comprising a sequence
CC encoding a human fibroblast growth factor (FGF)-like polypeptide. The
CC invention is useful to diagnose, prevent, treat or ameliorate diseases or
CC conditions associated with FGF-like polypeptide including epidermolysis
CC bullosa, chemotherapy-induced alopecia, male baldness, gastric and
CC duodenal ulcers, erosions of the stomach and oesophagus, inflammatory

CC bowel disease such as Crohn's disease, hyaline membrane disease of
CC premature infants, smoke inhalation, emphysema, hepatic cirrhosis and
CC thymic epithelial atrophy. The nucleic acids may also be used to map
CC locations of FGF-like gene and related genes on chromosomes. The present
XX sequence represents a human FGF protein.
SQ Sequence 209 AA;

Query Match 100.0%; Score 209; DB 8; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDTGFHSLWVSLVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQOTEAH 60
Db |||||
1 MDSDTGFHSLWVSLVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQOTEAH 60
QY 61 LEIREDTGVGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120
Db |||||
61 LEIREDTGVGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEA 120
QY 121 CSFRELLEDGYNVQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db |||||
121 CSFRELLEDGYNVQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 209
Db |||||
181 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 209

RESULT 6
ADL57123
ID ADL57123 standard; protein; 209 AA.
XX AC ADL57123;
XX 03-JUN-2004 (first entry)
XX Human NOV6h protein SEQ ID NO:68.
XX human; antidiabetic; anorectic; cardiant; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopachic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipaemic; gene therapy;
KW fibroblast growth factor receptor 4; FGR4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX Homo sapiens.

OS
XX
XX WO2004022723-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-US028141.
XX 09-SEP-2002; 2002US-0409145P.
PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX (CURA-) CURAGEN CORP.
XX
XX
PI Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;

XX WPI; 2004-315567/29.
DR N-FSDB; ADL57122.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX Claim 1; SEQ ID NO 68; 214pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic,
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, neurotropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipaemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor 1 precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.

XX Sequence 209 AA;

Query Match 97.1%; Score 203; DB 8; Length 209;
Best Local Similarity 100.0%; Pred. No. 5.9e-185;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GFHSLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQOTEAHLETRD 66
Db |||||
7 GFHSLWVSVLAGLLGACQAHPIPDSSPLLFQGGVQRVLYTDDAQOTEAHLETRD 66
QY 67 GTVGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126
Db |||||
67 GTVGAADQSPESLLQKALKPGVIQILGVKTSRFLCQRPDGCALYSLHFDPEACSFREL 126
QY 127 LLEDGYNVQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPPALPEPPGILAPOPP 186
Db |||||
127 LLEDGYNVQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPPALPEPPGILAPOPP 186
QY 187 DVGSSDPLSMVGPQGRSPSYAS 209
Db |||||
187 DVGSSDPLSMVGPQGRSPSYAS 209

CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
 CC stimulation, inhibition or proliferation of myocytes, smooth muscle
 CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
 CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
 CC derived cells and endothelial cells and inhibiting chondrosarcomas,
 CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
 CC results in bone formation useful for treating bone defects, fractures,
 CC osteoporosis and other deficiencies in bone structure and formation.
 CC zFGF11 is useful for treating disorders associated with diabetes
 CC mellitus, neural cell development or degeneration, amyotrophic lateral
 CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
 CC maintenance of neuronal differentiation and congenital disorders of the
 CC nervous system or lack of neuronal development, promoting angiogenesis
 CC and wound healing, for revascularisation in eye, complications related to
 CC poor circulation such as diabetic foot ulcers, improving cardiac
 CC function, modulating surfactant production in the lung epithelium, to
 CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
 CC events, particularly in the heart or brain and for inducing skeletal
 CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
 CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
 CC are useful for inhibiting disorders associated with kidney epithelium
 CC such as glomerulonephritis

XX Sequence 208 AA;

Query Match 90.0%; Score 188; DB 4; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.2e-170;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LLGACQAHPIPDSSPLQFGQVQRVLYTDDAQCTEAHLFIREDTGVGGADQSPESLL 81
 DB 21 LLGACQAHPIPDSSPLQFGQVQRVLYTDDAQCTEAHLFIREDTGVGGADQSPESLL 80
 QY 82 QLKALKPGVIOILGVKTSRFLCQPDGALYGSLLHFDPEACSFRELLLEDGYNVYQSEAHG 141
 DB 81 QLKALKPGVIOILGVKTSRFLCQPDGALYGSLLHFDPEACSFRELLLEDGYNVYQSEAHG 140
 QY 142 LPLHLPGNKSHPRDPA PRGPAPRFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSNVGVPSQ 201
 DB 141 LPLHLPGNKSHPRDPA PRGPAPRFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSNVGVPSQ 200
 QY 202 GRSPSYAS 209
 DB 201 GRSPSYAS 208

RESULT 10

AAU83630

ID AAU83630 standard; protein; 208 AA.

XX AC AAU83630;

XX DT 08-MAY-2002 (first entry)

XX DE Human PRO protein, Seq ID No 78.

XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.

XX OS Homo sapiens.

XX PN WO200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US021066.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220585P.

XX PR 25-JUL-2000; 2000US-0220605P.

XX PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 26-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-AUG-2000; 2000US-0222425P.
 PR 22-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0233646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABK33574.
 XX

One hundred and twenty two nucleic acids encoding PRO polypeptides,
 useful for treating a PRO related disorder and for diagnosing tumors such
 as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 or liver tumor.

Claim 11; Fig 78; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids
 encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 encode human secreted proteins. The PRO nucleic acids, polypeptides,
 agonists and antagonists are useful for treating a PRO related disorder.
 The PRO polypeptides are useful for diagnosing tumors, especially lung
 cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 liver tumor. The PRO polypeptides are useful for stimulating the
 proliferation of, or gene expression, in pericyte cells, for stimulating
 the proliferation or differentiation of chondrocyte cells, for
 stimulating the release of tumour necrosis factor-alpha from human blood,
 for stimulating or inhibiting the proliferation of normal human dermal
 fibroblast cells. The PRO polypeptide may also be used as molecular
 weight markers and for tissue typing. The PRO nucleic acids have
 applications in molecular biology, including use as hybridisation probes,
 and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 protein sequences of the invention

Sequence 208 AA;

Query Match 90.0%; Score 188; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.2e-170;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LLGACQAHPIPDSSPLQFGQVQRVLYTDDAQCTEAHLFIREDTGVGGADQSPESLL 81
 DB 21 LLGACQAHPIPDSSPLQFGQVQRVLYTDDAQCTEAHLFIREDTGVGGADQSPESLL 80
 QY 82 QLKALKPGVIOILGVKTSRFLCQPDGALYGSLLHFDPEACSFRELLLEDGYNVYQSEAHG 141
 DB 81 QLKALKPGVIOILGVKTSRFLCQPDGALYGSLLHFDPEACSFRELLLEDGYNVYQSEAHG 140
 QY 142 LPLHLPGNKSHPRDPA PRGPAPRFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSNVGVPSQ 201
 DB 141 LPLHLPGNKSHPRDPA PRGPAPRFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSNVGVPSQ 200
 QY 202 GRSPSYAS 209


```

Db      201 GRSPSYAS 208
|||||||
RESULT 11
ABG32359
ID      ABG32358 standard; protein; 208 AA.
XX
AC      ABG32358;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Human fibroblast growth factor (FGF) homologue, zFGF11.
XX
KW      Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR11c;
KW      osteoblastic lineage cell; diabetes mellitus; neuropathy;
KW      neural cell development; amyotrophic lateral sclerosis;
KW      cerebrovascular stroke; neuronal differentiation; congenital disorder;
KW      nervous system disorder; cardiac function; wound healing.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Peptide
FT      1..27
FT      /label= Signal_sequence
FT      Protein
FT      28..208
FT      /note= "Mature fibroblast growth factor homologue,
FT      zFGF11. This sequence is specifically claimed in claim 4"
XX
US2002081663-A1.
XX
PN      27-JUN-2002.
XX
PD      05-JAN-2001; 2001US-00755695.
XX
PF      05-JAN-2000; 2000US-0174526P.
XX
PR      (CONK/) CONKLIN D C.
XX      (CHEN/) CHEN Z.
XX
PA      Conklin DC, Chen Z;
XX
PI      WPI; 2002-626540/67.
XX      N-PSDB; ABK91310.
XX
PT      Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in
PT      treatment of disorders associated with diabetes mellitus, neural cell
PT      development or degeneration, amyotrophic lateral sclerosis,
PT      cerebrovascular stroke.
XX
PS      Claim 4; Fig 1; 35pp; English.
XX
CC      The invention relates to an isolated human polypeptide (I) for zFGF11 (a
CC      fibroblast growth factor), and the encoding polynucleotide (II). (I) and
CC      (II) are used in methods of the invention stimulating proliferation of
CC      mesenchymal cells, detecting the presence of zFGF11 in a biological
CC      sample, detecting the presence of FGFR11c in a biological sample and
CC      stimulating proliferation of osteoblastic lineage cells. The
CC      polypeptides, nucleic acid and/or antibodies of the invention may be used
CC      in treatment of disorders associated with diabetes mellitus, neural cell
CC      development or degeneration, amyotrophic lateral sclerosis,
CC      cerebrovascular stroke, neuropathy associated with lack of maintenance of
CC      neuronal differentiation, and congenital disorders of the nervous system
CC      or lack of neuronal development. Molecules of the invention may also be
CC      useful for improving cardiac function and for promoting wound healing of
CC      the epidermis. The present sequence represents the amino acid sequence of
CC      human zFGF11
XX
SQ      Sequence 208 AA;

Query Match      90.0%; Score 188; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-170;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22  LLGACQAHPIPDSSPLLQFGGVORXYLYTDDAQTEAHLREIDGTGVGGAADQSPSSL 81
Db      21  LLGACQAHPIPDSSPLLQFGGVORXYLYTDDAQTEAHLREIDGTGVGGAADQSPSSL 80
QY      82  QLKALKEGVIOILGVKTSRFLCQRPDGLYGSLLHFDPEACSFRELLEDGYNVYQSEAHG 141
Db      81  QLKALKEGVIOILGVKTSRFLCQRPDGLYGSLLHFDPEACSFRELLEDGYNVYQSEAHG 140
QY      142  LPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGILAPQPPDVCGSSDPLSMVGPSQ 201
Db      141  LPLHLPGNKSPHRDPAPRGPARFLPLFGLPPALPEPPGILAPQPPDVCGSSDPLSMVGPSQ 200
QY      202  GRSPSYAS 209
Db      201  GRSPSYAS 208

RESULT 12
AAE17601
ID      AAE17601 standard; protein; 208 AA.
XX
AC      AAE17601;
XX
DT      22-APR-2002 (first entry)
XX
DE      Human extracellular messenger (XMES)-3 protein.
XX
KW      Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;
KW      Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
KW      acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
KW      developmental disorder; anaemia; Cushing's syndrome; endocrine disorder;
KW      vascular malformation; cell proliferative disorder; gene therapy; cancer;
KW      neuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic;
KW      hyperthyroidism; gonadal steroid hormone; pancreatic disorder; neotropic;
KW      diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
KW      antiviral; antifungal; parasitic; protozoal; allergy.
XX
OS      Homo sapiens.
XX
PN      WO200194587-A2.
XX
PD      13-DEC-2001.
XX
PF      06-JUN-2001; 2001WO-US018476.
XX
PR      06-JUN-2000; 2000US-0210233P.
PR      23-JUN-2000; 2000US-0213465P.
PR      14-NOV-2000; 2000US-0249019P.
XX
PA      (INCY-) INCYTE GENOMICS INC.
XX
PI      Lal P, Yue H, He A, Nguyen DB, Wallia N, Gandhi AR, Azimzai Y;
PI      Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BW, Lee S, Hafalia A;
PI      Policky JL;
XX
DR      WPI; 2002-154573/20.
DR      N-PSDB; AAD28493.
XX
PT      New extracellular messenger polypeptides and polynucleotides encoding
PT      them, useful for diagnosing, treating or preventing e.g. neurological,
PT      autoimmune, inflammatory, developmental and endocrine disorders.
XX
PS      Claim 1; Page 11; 123pp; English.
XX
CC      The present invention relates to new extracellular messenger polypeptides
CC      and polynucleotides encoding them. XMES is useful in the diagnosis,
CC      treatment and prevention of neurological disorders (e.g. epilepsy,
CC      stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g.
CC      acquired immune deficiency syndrome, AIDS, Addison's disease, or
CC      allergies), developmental disorders (e.g. renal tubular acidosis, anaemia
CC      or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy,
CC      aneurysm or vascular malformation), and cell proliferative disorders

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CC (e.g. cancer), and in the assessment of the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC extracellular messengers. XMEs may also be used in the treatment of
CC viral, bacterial, fungal, parasitic, protozoal and helminthic
CC infections, trauma, disorders associated with hypopituitarism,
CC hypothyroidism, hyperthyroidism or gonadal steroid hormones, and
CC pancreatic disorders such as type I or type II diabetes mellitus. The
CC sequence is human XMEs-3 protein
XX
SQ Sequence 208 AA;

Query Match 90.0%; Score 188; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-170;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQTEAHLEIREDTGTVGGAADQSPESLL 81
Db 21 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQTEAHLEIREDTGTVGGAADQSPESLL 80
QY 82 QLKALKPGVQIILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHG 141
Db 81 QLKALKPGVQIILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHG 140
QY 142 LPLHLPGNKSPhRDPAHPGPARFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQS 201
Db 141 LPLHLPGNKSPhRDPAHPGPARFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQS 200
QY 202 GRSPSYAS 209
Db 201 GRSPSYAS 208

RESULT 13
ABU80777
ID ABU80777 standard; protein; 208 AA.
XX
AC ABU80777;
DT 23-JUN-2003 (first entry)
DE Human PRO polypeptide #39.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
OS Homo sapiens.
XX
FN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-342045/32.
DR N-PSDB; ACA66879.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 78; 314pp; English.
XX

CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 208 AA;

Query Match 90.0%; Score 188; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-170;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQTEAHLEIREDTGTVGGAADQSPESLL 81
Db 21 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQTEAHLEIREDTGTVGGAADQSPESLL 80
QY 82 QLKALKPGVQIILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHG 141
Db 81 QLKALKPGVQIILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHG 140
QY 142 LPLHLPGNKSPhRDPAHPGPARFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQS 201
Db 141 LPLHLPGNKSPhRDPAHPGPARFLPLPGLPPALPEPPGILAPQPPDVGVSSDPLSMVGPQS 200
QY 202 GRSPSYAS 209
Db 201 GRSPSYAS 208

RESULT 14
ABO33743
ID ABO33743 standard; protein; 208 AA.
XX
AC ABO33743;
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX
OS Homo sapiens.
XX
FN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-512315/48.
DR N-PSDB; ACD68631.
XX

PT New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.

XX Claim 11; Fig 78; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any of these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

XX Sequence 208 AA;

Query Match 90.0%; Score 188; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-170;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQQTAEHLREIDGTGGADQSPESLL 81

Db 21 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQQTAEHLREIDGTGGADQSPESLL 80

QY 82 QLKALKPGVIOILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLLEDGNNVQSEAHG 141

Db 81 QLKALKPGVIOILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLLEDGNNVQSEAHG 140

QY 142 LPLHLPGNKSHPDRPAPRGPARFLPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPSQ 201

Db 141 LPLHLPGNKSHPDRPAPRGPARFLPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPSQ 200

QY 202 GRSPSYAS 209

Db 201 GRSPSYAS 208

RESULT 15

ABU82086

ID ABU82086 standard; protein; 208 AA.

XX AC ABU82086;

XX DT 25-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;

KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX Homo sapiens.

XX US2003088063-A1.

XX 08-MAY-2003.

XX 12-AUG-2002; 2002US-00219003.

XX 25-JUL-2000; 2000US-0220664P.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-393229/37.

XX N-PSDB; ACA68535.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 78; 314pp; English.

XX The invention describes one hundred and eighty seven nucleic acids
XX encoding novel human secreted and transmembrane (PRO) polypeptides. The
XX PRO nucleic acids, polypeptides, agonists and antagonists are useful for
XX treating or diagnosing a cardiovascular, endothelial or angiogenic
XX disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
XX related macular degeneration, atherosclerosis, hypertension, arterial
XX restenosis, rheumatoid arthritis, angina, myocardial infarctions,
XX thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
XX carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
XX have applications in molecular biology, including use as hybridisation
XX probes, and in chromosome and gene mapping. This is the amino acid
XX sequence of a novel human secreted and transmembrane PRO polypeptide

XX Sequence 208 AA;

Query Match 90.0%; Score 188; DB 6; Length 208;

Best Local Similarity 100.0%; Pred. No. 1.2e-170; Indels 0; Gaps 0;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQQTAEHLREIDGTGGADQSPESLL 81

Db 21 LLGACQAHPIPDSSPLLPFGGQVRQRYLYTDDAQQTAEHLREIDGTGGADQSPESLL 80

QY 82 QLKALKPGVIOILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLLEDGNNVQSEAHG 141

Db 81 QLKALKPGVIOILGVKTSRFLCQRPDGLYGLSLHFDPEACSFRELLLEDGNNVQSEAHG 140

QY 142 LPLHLPGNKSHPDRPAPRGPARFLPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPSQ 201

Db 141 LPLHLPGNKSHPDRPAPRGPARFLPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPSQ 200

QY 202 GRSPSYAS 209

Db 201 GRSPSYAS 208

Search completed: July 8, 2005, 22:50:44

Job time : 165 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:21:15 ; Search time 177 Seconds
(without alignments)
604.658 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 209

Sequence: 1 MDSDETFEHSGLMWSVLG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table:  Gapop 60:0 , Gapext 60:0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	100.0	209	1 FGFL HUMAN	Q9nsal homo sapien
2	173	82.8	209	2 Q9N683	Q9ns63 homo sapien
3	30	14.4	210	1 FGFL MOUSE	Q9ijn1 mus musculus
4	21	10.0	208	2 Q9V180	Q8vi80 rattus norv
5	10	4.8	141	2 Q9DUC8	Q9duc8 tt virus. o
6	9	4.3	136	2 Q9DUC5	Q9duc5 tt virus. o
7	9	4.3	157	2 Q5YWB0	Q5ywb0 oryza sativ
8	9	4.3	671	1 HPP2 METAC	Q8tja8 methanosarc
9	8	3.8	51	2 Q6MSV7	Q6msv7 mycoplasma
10	8	3.8	220	2 Q7NWZ2	Q7nwz2 chromobacte
11	8	3.8	301	2 Q98I00	Q98i00 rhizobium 1
12	8	3.8	474	2 Q8H462	Q8h462 oryza sativ
13	8	3.8	493	2 Q7NHU7	Q7nhu7 gloeobacter
14	8	3.8	499	2 Q6NFF0	Q6nff0 corynebacte
15	8	3.8	523	2 Q82G38	Q82g38 streptomyce
16	8	3.8	568	2 Q9RWU8	Q9rwu8 deinococcus
17	8	3.8	584	2 Q84A53	Q84a53 chlamydia t
18	8	3.8	666	2 P90898	P90898 caenorhabdi
19	8	3.8	747	2 Q9PAD1	Q9pad1 xanthomonas
20	8	3.8	1062	2 Q63ZY4	Q63zy4 homo sapien
21	8	3.8	1075	1 ATXL HUMAN	Q8wmw7 homo sapien
22	8	3.8	1670	1 CLOT_PENMO	Q9u572 penaeus mon
23	7	3.3	46	2 Q7SMG6	Q7smg6 homo sapien
24	7	3.3	52	2 Q8NRN9	Q8nrn9 streptomyce
25	7	3.3	63	2 Q82PW9	Q82pw9 streptomyce
26	7	3.3	73	2 Q7NT52	Q7nt52 chromobacte
27	7	3.3	73	2 Q7VU89	Q7vu89 bordetella
28	7	3.3	73	2 Q7W4S6	Q7w4s6 bordetella
29	7	3.3	73	2 Q7WGA2	Q7wga2 bordetella
30	7	3.3	90	2 Q9RTB8	Q9rtb8 deinococcus
31	7	3.3	92	2 Q51557	Q51557 pseudomonas

32	7	3.3	93	2	Q64RH3	Q64rh3 bacteroides
33	7	3.3	100	2	Q89JN3	Q89jn3 bradyrhizob
34	7	3.3	116	2	Q639B1	Q639b1 bacillus ce
35	7	3.3	116	2	Q81NH6	Q81nh6 bacillus th
36	7	3.3	116	2	Q6HGM4	Q6hgm4 bacillus th
37	7	3.3	117	2	Q8RJH9	Q8rjh9 streptomyce
38	7	3.3	118	2	Q6V9G4	Q6v9g4 plasmodium
39	7	3.3	118	2	Q6V9G6	Q6v9g6 plasmodium
40	7	3.3	119	2	Q9MEX3	Q9mex3 lepilemur d
41	7	3.3	119	2	Q9MEY8	Q9mey8 lepilemur d
42	7	3.3	120	2	Q9NS32	Q9ns32 homo sapien
43	7	3.3	120	2	Q41115	Q41115 paramacium
44	7	3.3	123	2	Q6V9G9	Q6v9g9 plasmodium
45	7	3.3	123	2	Q7XLT5	Q7xlt5 oryza sativ

ALIGNMENTS

RESULT 1
ID FGFL HUMAN STANDARD; PRT; 209 AA.
AC Q9NSA1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).
GN Name=FGF21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE OF 29-43.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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or send an email to license@ebi-sib.ch).

DR EMBL; AB021975; BAA99415.1; -;
 DR EMBL; AY359086; AAQ99444.1; -;
 DR HSSP; P03968; IBAR.
 DR Genew; HGNC:3678; FGF21.
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR002209; HB/F growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HBGFFGF.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR PROSITE; PS00247; HBGFFGF; FALSE NEG.
 KW Direct protein sequencing; Growth factor; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 209 Fibroblast growth factor-21.
 FT CONFLICT 23 23 Missing (in Ref. 2).
 SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;
 Query Match 100.0%; Score 209; DB 1; Length 209;
 Best Local Similarity 100.0%; Pred. No. 1.6e-201;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSDTGFHSLVWVSLAGLLGACQAHPIPDSSPLLOFGQVQRVLYTDDAQQTAAH 60
 DB 1 MDSDTGFHSLVWVSLAGLLGACQAHPIPDSSPLLOFGQVQRVLYTDDAQQTAAH 60
 QY 61 LEIREDTGVGAADQSPESLLQKALPGVLIQLGVKTSRFLCORPDGALYGSLLHFDEA 120
 DB 61 LEIREDTGVGAADQSPESLLQKALPGVLIQLGVKTSRFLCORPDGALYGSLLHFDEA 120
 QY 121 CSFRELLEDGVNYVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPPLP 180
 DB 121 CSFRELLEDGVNYVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPPLP 180
 QY 181 LAPQPPDVGSDDPLSMVGPSQGRSPSYAS 209
 DB 181 LAPQPPDVGSDDPLSMVGPSQGRSPSYAS 209
 RESULT 2
 QBN683
 ID QBN683 PRELIMINARY; PRT; 209 AA.
 AC QBN683;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Fibroblast growth factor 21.
 GN Name=FGF21;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=223188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
 RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
 DR EMBL; BC018404; AAH18404.1; -;
 DR HSSP; O95750; IPWA.
 DR GO; GO:0008083; P:growth factor activity; IEA.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR002209; HB/F growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HBGFFGF.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 KW Growth factor.
 SQ SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;
 Query Match 82.8%; Score 173; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 2.7e-165;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSDTGFHSLVWVSLAGLLGACQAHPIPDSSPLLOFGQVQRVLYTDDAQQTAAH 60
 DB 1 MDSDTGFHSLVWVSLAGLLGACQAHPIPDSSPLLOFGQVQRVLYTDDAQQTAAH 60
 QY 61 LEIREDTGVGAADQSPESLLQKALPGVLIQLGVKTSRFLCORPDGALYGSLLHFDEA 120
 DB 61 LEIREDTGVGAADQSPESLLQKALPGVLIQLGVKTSRFLCORPDGALYGSLLHFDEA 120
 QY 121 CSFRELLEDGVNYVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPPLP 173
 DB 121 CSFRELLEDGVNYVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPPLP 173
 RESULT 3
 FGFL MOUSE
 ID FGFL MOUSE STANDARD; PRT; 210 AA.
 AC Q9JUN1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fibroblast growth factor-21 precursor (FGF-21).
 GN Name=FGF21;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;
 RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
 RT "Identification of a novel FGF, FGF-21, preferentially expressed in
 the liver.";
 RL Biochim. Biophys. Acta 1492:203-206(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaudo I., Oeato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grummond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmern A., Carninci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Iehi Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUES-Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also
CC expressed in the thymus at lower levels.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -----
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CC -----
DR EMBL; AB025718; BAA99416.1; -;
DR EMBL; AK007574; BAB25115.1; -;
DR EMBL; BC049592; AAH49592.1; -;
DR HSP; P08620; I17T;
DR MGD; MGI:1861377; Fgf21.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002209; HB/F growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.

DR SMART; SM00442; FGF; 1.
KW PROSITE; PS00247; HBGF_FGF; FALSE NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 210 Fibroblast growth factor-21.
SQ SEQUENCE 210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;
Query Match 14.4%; Score 30; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 115 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 144
DB 116 HFDPEACSFRELLLEDGYNVYQSEAHGLPL 145
RESULT 4
OSV180 PRELIMINARY; PRT; 208 AA.
ID Q8V180
AC Q8V180;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
GN Name=FGF21;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RA Itoh N.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR EMBL; AB078901; BAB84299.1; -;
DR HSP; O95750; 1PWA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFPGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
KW Growth factor.
SQ SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;
Query Match 10.0%; Score 21; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 DSSPLQFGGQVRQRYLYTDD 53
DB 34 DSSPLQFGGQVRQRYLYTDD 54
RESULT 5
Q9DUC8
ID Q9DUC8 PRELIMINARY; PRT; 141 AA.
AC Q9DUC8
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE ORF2.
GN Name=ORF2;
OS TT virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20534983; PubMed=11080484; DOI=10.1006/viro.2000.0588;
RA Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
RA Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
RT "Species-specific TT viruses in humans and nonhuman primates and their
RT phylogenetic relatedness.";

```

RL Virology 277:368-378 (2000).
DR EMBL; AB041958; BAB19309.2; -.
DR InterPro; IPR004118; TT_ORF2.
DR Pfam; PF02957; TT_ORF2; 1.
SQ SEQUENCE 141 AA; 14433 MW; 90FE7833DBAC0A04 CRC64;
      Query Match      4.8%; Score 10; DB 2; Length 141;
      Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 RFLPLPGLP 172
Db 84 RFLPLPGLP 93

RESULT 6
ID Q9DUC5 PRELIMINARY; PRT; 136 AA.
AC Q9DUC5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF2.
DE "Species-specific TT viruses in humans and nonhuman primates and their phylogenetic relatedness."
GN EMBL; AB041959; BAB19312.1; -.
GN InterPro; IPR004118; TT_ORF2.
GN Pfam; PF02957; TT_ORF2; 1.
SQ SEQUENCE 136 AA; 14088 MW; 91C43BEPFC5CB22B1 CRC64;
      Query Match      4.3%; Score 9; DB 2; Length 136;
      Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 RFLPLPGLP 171
Db 75 RFLPLPGLP 83

RESULT 7
ID Q6YWB0 PRELIMINARY; PRT; 157 AA.
AC Q6YWB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0501509.24 (Hypothetical protein P0584E12.51).
DE Name=P0501E09.24; Synonyms=P0584E12.51;
GN Oryza sativa (japonica cultivar-group).
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
KW EMBL; AP005787; BAD17576.1; -.

DR EMBL; AP005591; BAD17409.1; -.
KW Hypothetical protein.
SQ SEQUENCE 157 AA; 16544 MW; 9F9A97BB5BD05B18 CRC64;
      Query Match      4.3%; Score 9; DB 2; Length 157;
      Best Local Similarity 100.0%; Pred. No. 2;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 PIPDSSPLL 38
Db 22 PIPDSSPLL 30

RESULT 8
ID HPP2_METAC STANDARD; PRT; 671 AA.
AC Q8TJA8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pyrophosphate-energized proton pump 2 (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase 2) (H+-PPase 2) (Membrane-bound proton-translocating pyrophosphatase 2).
DE Name=hppA2; OrderedLocNames=MA3880;
GN Methanosarcina acetivorans.
OS Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nisbaum C., Roy A., Endrizzi M.G., Macdonald P., Brown A., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Johnson R., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirelli A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."
RL Genome Res. 12:532-542(2002).
CC -!- FUNCTION: Generates a proton motive force; it probably catalyzes a fully reversible reaction, thus being able to synthesize pyrophosphate when the proton motive force is sufficient (By similarity).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase (TC 3.A.10) family. Subfamily 2.
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EMBL; AE011099; AAM07231.1; -.
HAMAP; MF_01130; -; 1.
InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR PIRSF; PIRSF001265; H+-PPase; 1.
DR TIGRFAMs; TIGR01104; V_PPase; 1.
KW Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium; Transmembrane.
```

FT TRANSMEM 5 27 Potential.
 FT TRANSMEM 57 74 Potential.
 FT TRANSMEM 79 101 Potential.
 FT TRANSMEM 122 144 Potential.
 FT TRANSMEM 154 176 Potential.
 FT TRANSMEM 227 244 Potential.
 FT TRANSMEM 248 270 Potential.
 FT TRANSMEM 282 301 Potential.
 FT TRANSMEM 311 333 Potential.
 FT TRANSMEM 354 376 Potential.
 FT TRANSMEM 391 413 Potential.
 FT TRANSMEM 490 512 Potential.
 FT TRANSMEM 553 575 Potential.
 FT TRANSMEM 580 599 Potential.
 FT TRANSMEM 644 666 Potential.
 FT SITE 451 451
 FT SEQUENCE 671 AA; 69016 MW; 45843BD57F4B30F7 CRC64;
 Query Match 4.3%; Score 9; DB 1; Length 671;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 VLGLLLGA 25
 Db 491 VLGLLLGA 499
 RESULT 9
 Q6MSV7 PRELIMINARY; PRT; 51 AA.
 AC Q6MSV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical transmembrane protein.
 GN OrderedLocusNames=MSC_0860;
 OS Mycoplasma mycoides (subsp. mycoides SC).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=44101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PGI;
 RX PubMed=14762060; DOI=10.1101/gr.1673304;
 RA Westberg J., Persson A., Holmberg A., Goessmann A., Lundeberg J.,
 RA Johansson K.-E., Pettersson B., Uhlen M.;
 RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
 RT strain PGI, the causative agent of contagious bovine pleuropneumonia
 RT (CBPP).";
 RL Genome Res. 14:221-227(2004).
 DR EMBL; BX842644; CAF77281.1;
 KW Complete proteome.
 SQ SEQUENCE 51 AA; 5726 MW; ACE712AD7AFA6F7C CRC64;
 Query Match 3.8%; Score 8; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 VLGLLLG 24
 Db 30 VLGLLLG 37
 RESULT 10
 Q7NWZ2 PRELIMINARY; PRT; 220 AA.
 AC Q7NWZ2;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable transcriptional regulator, Tetr family.
 GN OrderedLocusNames=CV1837;
 OS Chromobacterium violaceum.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Faicao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyza M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa P.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Rondinelli E.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;
 RA "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 CC -1- SIMILARITY: Contains 1 HTH tetR-type DNA-binding domain.
 DR EMBL; AB016916; AAQ59511.1;
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR009057; Homeodomain_like.
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; Tetr_N; 1.
 DR PRINTS; PR00455; HTH_Tetr.
 KW Complete proteome; DNA-binding; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 220 AA; 23672 MW; 2D7C2751D0138968 CRC64;
 Query Match 3.8%; Score 8; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 ELLLEDGY 132
 Db 36 ELLLEDGY 43
 RESULT 11
 Q98100 PRELIMINARY; PRT; 301 AA.
 ID Q98100;
 AC Q98100;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mlr2632 protein.
 GN OrderedLocusNames=mlr2632;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099; PubMed=11214968;
 RX MEDLINE=21082930; PubMed=11214968;


```
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuura A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AF003000; BAB49716.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6; 2.
KW Complete proteome.
SQ SEQUENCE 301 AA; 31470 MW; C7E91DB86D02658B CRC64;

Query Match 3.8%; Score 8; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 LAGLLIGA 25
Db 122 LAGLLIGA 129

RESULT 12
QBH462 PRELIMINARY; PRT; 474 AA.
AC QBH462;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative Flavonol 3-O-glucosyltransferase (UDP-glucose flavonoid 3-O-
DE glucosyltransferase).
GN Name=P0470D12.134;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
RT clone:P0470D12."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the UDP-glucosyltransferase family.
DR EMBL; AP004300; BAC15998.1; -.
DR Gramene; Q8H462; -.
DR GO; GO:0016759; P:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_Glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 474 AA; 50978 MW; EE1782C36B35E21 CRC64;

Query Match 3.8%; Score 8; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LPGLPPAL 174
Db 74 LPGLPPAL 81

RESULT 13
Q7NHU7 PRELIMINARY; PRT; 493 AA.
AC Q7NHU7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glr2438 protein.
```

```
GN OrderedLocusNames=g1r2438;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuura A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC EMBL; AP006576; BAC90379.1; -.
DR EMBL; AP006576; BAC90379.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR001775; Bac_GSPD.
DR InterPro; IPR004846; GSP1/IIIProtein.
DR InterPro; IPR005644; NOLW-like.
DR Pfam; PF00263; Secretin; 1.
DR Pfam; PF03958; Secretin N; 1.
DR PRINTS; PR00811; BCTERIALGSPD.
KW Complete proteome; Transport.
KW SEQUENCE 493 AA; 51946 MW; 5893096AADAF9C0C CRC64;

Query Match 3.8%; Score 8; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 GTVGGAAD 74
Db 264 GTVGGAAD 271

RESULT 14
Q6NFF0 PRELIMINARY; PRT; 499 AA.
AC Q6NFF0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=DIP1941;
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cerdeno-Tarraga A.-M., Efstathiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Beara G.S., Churcher C.M., James K.D.,
RA De Zorja A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129."
RL Nucleic Acids Res. 31:6516-6523(2003).
DR EMBL; BX248359; CAES0475.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 499 AA; 52943 MW; B39A06AAD519A0DA CRC64;
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Query Match 3.8%; Score 8; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLAGLLG 24
|||
DB 70 VLAGLLG 77

RESULT 15

Q82G38 PRELIMINARY; PRT; 523 AA.
AC Q82G38;
DT 01-JUN-2003 (TREMREL. 24, Created)
DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE Putative ABC transporter transmembrane protein.
GN OrderedLocusNames=SAV4060;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005037; BAC71772.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000169; Pept_cys_acsite.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW Complete proteome; Transmembrane_
SQ SEQUENCE 523 AA; 55097 MW; 62E41DAF43D0826B CRC64;

Query Match 3.8%; Score 8; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LAGLLGA 25
|||
DB 254 LAGLLGA 261

Search completed: July 8, 2005, 22:47:55
Job time : 181 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 22:03:50 ; Search time 3.6875 Seconds
(without alignments)
391.390 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	58.4	1173	T31421	C-terminal domain-
2	50	56.2	165	G72619	hypothetical prote
3	48	53.9	492	C72417	sugar kinase, FGGY
4	46	51.7	723	VCFVPP	coat protein VP1 -
5	46	51.7	729	A60006	coat protein VP1 -
6	46	51.7	729	VCFVNA	probable carbohydr
7	45	50.6	517	AG0157	collagen alpha 2(I
8	45	50.6	618	S32436	EIN2 protein - Ara
9	45	50.6	1294	T48349	probable purine nu
10	44.5	50.0	545	S46151	GHI protein - soyb
11	44	49.4	339	T05726	colony-stimulating
12	44	49.4	552	S35703	macrophage colony-
13	44	49.4	552	A31401	CTP synthase (EC 6
14	44	49.4	590	S72961	hypothetical prote
15	43	48.3	105	C72631	probable aldehyde
16	43	48.3	280	T35432	beta-ketoacyl synt
17	43	48.3	407	S25841	anti-mullerian hor
18	43	48.3	573	JC4335	hypothetical prote
19	43	48.3	779	T21021	hypothetical prote
20	43	48.3	781	T41551	collagen alpha 1(V
21	43	48.3	920	A45748	ATP-dependent perm
22	43	48.3	1049	S19421	hypothetical prote
23	42	47.2	278	T35379	3-isopropylmalate
24	42	47.2	355	T31128	hypothetical prote
25	42	47.2	520	QOCV65	hypothetical prote
26	42	47.2	522	QOCV65	inclusion body mat
27	42	47.2	522	S06092	probable anti-mull
28	42	47.2	557	S41627	mullerian-inhibiti
29	42	47.2	568	JC5629	

30	42	47.2	818	2	T02436	proline-rich prote
31	42	47.2	1043	2	T13172	gag-like protein p
32	41.5	46.6	240	2	C86194	hypothetical prote
33	41.5	46.6	324	2	S44956	lmbi protein - Str
34	41.5	46.6	392	1	FOLJGA	gag polyprotein -
35	41.5	46.6	392	1	FOLJGB	gag polyprotein -
36	41.5	46.6	393	2	S29356	gag protein - bovi
37	41.5	46.6	1174	2	T49868	related to suppress
38	41	46.1	111	2	H82597	hypothetical prote
39	41	46.1	117	2	T47161	hypothetical prote
40	41	46.1	118	2	S54309	hypothetical 13.2K
41	41	46.1	282	2	A85076	hypothetical prote
42	41	46.1	312	1	Q08E07	US10 protein - hum
43	41	46.1	413	2	T31663	isoleucine-tRNA li
44	41	46.1	520	1	QOCV6C	hypothetical prote
45	41	46.1	520	2	JN0498	hypothetical 58K p

ALIGNMENTS

RESULT 1

T31421

C-terminal domain-binding protein xA1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T31421

R:Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord

Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996

A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit

A:Reference number: Z21024; MUID:96293459; PMID:8692929

A:Accession: T31421

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1173 <YUR>

A:Cross-references: UNIPROT:Q63624; EMBL:U49056; NID:G1439531; PID:G1439532; PIDN:AACS26

A:Experimental source: hippocampus

Query Match 58.4%; Score 52; DB 2; Length 1173;

Best Local Similarity 66.7%; Pred. No. 5.9;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14

DB 224 PGDDSPHREPPP 235

RESULT 2

G72619

hypothetical protein APE1416 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: G72619

R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: G72619

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <KAW>

A:Cross-references: UNIPROT:Q9YC35; DBJ:AP000061; NID:G5104821; PIDN:BAA80413.1; PID:d1

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1416

C:Superfamily: Aeropyrum pernix hypothetical protein APE1416

Query Match 56.2%; Score 50; DB 2; Length 165;

Best Local Similarity 68.8%; Pred. No. 1.5;

Matches 11; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 LPGNK--SPHRDPAPR 15

Db 140 LPANRSGSPHRDPAPR 155

RESULT 3
C72417
sugar kinase, FGGY family - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72417
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <ARN>
A:Cross-references: UNIPROT:Q9WXX1; GB:AE001697; GB:AE000512; NID:G4980597; PIDN:AAD3521
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0116
C:Superfamily: xylulokinase

Query Match 53.9%; Score 48; DB 2; Length 492;
Best Local Similarity 53.3%; Pred. No. 9.8;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HLPNGKSPHRDPAPR 15
Db 340 YLNGERTPHRDPAPR 354

RESULT 4
VCPVPP
coat protein VP1 - porcine parvovirus
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B33302
R:Ranz, A.I.; Mancus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A:Title: Porcine parvovirus: DNA sequence and genome organization.
A:Reference number: A33302; MUID:90010964; PMID:2794971
A:Accession: B33302
A:Molecule type: DNA
A:Residues: 1-723 <RAN>
A:Cross-references: UNIPROT:P18546; EMBL:D00623
C:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:145-723/Product: coat protein VP2 #status predicted <VP2>

Query Match 51.7%; Score 46; DB 1; Length 723;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGKSPHRDPAPR 15
Db 111 PGSKPPGKRPPAPR 123

RESULT 5
A60006
coat protein VP1 - porcine parvovirus (strain 90HS)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A60006
R:Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.

Virus Res. 13, 79-86, 1989
A:Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A:Reference number: A60006; MUID:89319168; PMID:2750278
A:Accession: A60006
A:Molecule type: DNA
A:Residues: 1-729 <SAK>
A:Cross-references: UNIPROT:P33484
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; Glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #status predicted <VP2>

Query Match 51.7%; Score 46; DB 1; Length 729;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGKSPHRDPAPR 15
Db 117 PGSKPPGKRPPAPR 129

RESULT 6
VCPVNA
coat protein VP1 - porcine parvovirus (strain NADL-2)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: B33743; D48472
R:Vasudevaacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 173, 368-377, 1989
A:Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal pa
A:Reference number: A33743; MUID:90085785; PMID:2596019
A:Accession: B33743
A:Molecule type: DNA
A:Residues: 1-729 <VAS>
A:Cross-references: UNIPROT:P18546; GB:M32787; NID:G332983; PIDN:AAA46917.1; PID:G332983
R:Bergeron, J.; Meneses, J.; Tijssen, P.
Virology 197, 86-98, 1993
A:Title: Genomic organization and mapping of transcription and translation products of t
A:Reference number: A48472; MUID:94025614; PMID:8212598
A:Accession: D48472
A:Molecule type: DNA
A:Residues: 11-729 <BER>
A:Experimental source: NADL-2, ATCC VR-742
A:Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBI:P138794)
C:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; Glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 51.7%; Score 46; DB 1; Length 729;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGKSPHRDPAPR 15
Db 117 PGSKPPGKRPPAPR 129

RESULT 7
AG0157
probable carbohydrate kinase YPO1291 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG0157
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

Db 518 PGKQGP HGH PGPR 530

A;Reference number: Z15436
A;Accession: T05726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-339 <HAG>
A;Cross-references: UNIPROT:Q22465; EMBL:AF016633; NID:g2388688; PIDN:AAB70005.1; PID:g2388688; MUID:85242709; PMID:3925458
A;Experimental source: cultivar Wayne
C;Genetics:
A;Gene: GH1
C;Superfamily: auxin-induced protein aux28

Query Match 49.4%; Score 44; DB 2; Length 339;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LFGNKSPPHDP 12
| : : : : :
Db 62 LFGSQSPERP 72

RESULT 12
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35703
R;Borycki, A.G.; Lenormand, J.L.; Guillier, M.; Leibovitch, S.A.
Biochim. Biophys. Acta 1174, 143-152, 1993
A;Title: Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. Pos
A;Reference number: S35703; MUID:93363632; PMID:8357831
A;Accession: S35703
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-552 <BOR>
A;Cross-references: EMBL:M84361; NID:G203640; PIDN:AAA03032.1; PID:G203641
C;Superfamily: macrophage colony-stimulating factor

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGNKSPPHDP 14
| : : : : :
Db 202 PASASPHQPPAP 213

RESULT 13
A;Title: macrophage colony-stimulating factor precursor - mouse
N;Alternate names: colony-stimulating factor 1; M-CSF
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A31401; JN0294; A26575; A23166; A25883
R;Ladner, M.B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.; St
Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A;Title: cDNA cloning and expression of murine macrophage colony-stimulating factor from
A;Reference number: A31401; MUID:88320507; PMID:2457916
A;Accession: A31401
A;Molecule type: mRNA
A;Residues: 1-552 <LAD>
A;Cross-references: UNIPROT:P07141; GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1;
R;Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H.E.
Gene 102, 165-170, 1991
A;Title: Cloning and characterization of the murine promoter for the colony-stimulating
A;Reference number: JN0294; MUID:91340149; PMID:1874443
A;Accession: JN0294
A;Molecule type: DNA
A;Residues: 1-13 <HAR>
A;Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
R;Delamarter, J.F.; Hesston, C.; Semon, D.; Gough, N.M.; Rotherbuhler, R.; Mermod,
Nucleic Acids Res. 15, 2389-2390, 1987
A;Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A;Reference number: A26575; MUID:87174763; PMID:3494232

A;Accession: A26575
A;Molecule type: mRNA
A;Residues: 1-5, R', 7-245, A', 247-552
R;Ben-Avram, C.M.; Shively, J.E.; Shaddock, R.K.; Waheed, A.; Rajavashisth, T.; Lusis, A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A;Reference number: A23166; MUID:85242709; PMID:3925458
A;Accession: A23166
A;Molecule type: protein
A;Residues: 33-39, CC', 42-57 <BEN>
R;Rajavashisth, T.B.; Eng, R.; Shaddock, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A;Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulating f.
A;Reference number: A25883; MUID:87147232; PMID:3493488
A;Accession: A25883
A;Molecule type: mRNA
A;Residues: 1-2, 4-5, RPR', 9-100 <RAJ>
A;Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801
C;Superfamily: macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-552/Product: macrophage colony-stimulating factor #status predicted <MAT>
F;154,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PGNKSPPHDP 14
| : : : : :
Db 202 PASASPHQPPAP 213

RESULT 14
CTP synthase (BC 6.3.4.2) pyrG - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72961
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid L247.
A;Reference number: S72589
A;Accession: S72961
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <SMI>
A;Cross-references: UNIPROT:P53529; EMBL:U00021; NID:g467141; PIDN:AAA50916.1; PID:g467141
C;Genetics:
A;Start codon: GTG
C;Superfamily: CTP synthase
C;Keywords: ligase

Query Match 49.4%; Score 44; DB 2; Length 590;
Best Local Similarity 45.0%; Pred. No. 49;
Matches 9; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 HLPGNKSPHRD-----PAP 14
| : : : : :
Db 567 HLPNNSNQHRDGVRSFPAP 586

RESULT 15
CT2631
hypochemical protein APE1506 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: CT2631
R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: CT2631

A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-105 <KAW>
A:Cross-references: UNIPROT:Q9YBU3; DDBJ:AP000061; NID:g5104821; PIDN:BAA80505.1; PID:dl
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1506

Query Match 48.3%; Score 43; DB 2; Length 105;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 HLPGNKSPHRDP 12
||| ||: ||
Db 56 HLPNNKASHKLP 67

Search completed: July 8, 2005, 22:21:07
Job time : 5.6875 secs

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OM protein - protein search, using sw model

Run on: July 8, 2005, 21:54:48 ; Search time 18.0625 Seconds
(without alignments)
425.256 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	209	1 FGFL_HUMAN	Q9nsal homo sapien
2	89	100.0	209	2 Q8N683	Q8N683 homo sapien
3	52	58.4	1173	2 Q63624	Q63624 rattus norv
4	50	56.2	165	2 Q9YC35	Q9YC35 aeropyrum p
5	48	53.9	355	2 Q9SSY2	Q9SSY2 cucumis eat
6	48	53.9	492	2 Q9WXX1	Q9WXX1 thermotoga
7	48	53.9	574	2 Q9BLT0	Q9BLT0 leishmania
8	48	53.9	601	1 SYQ_RHOBA	Q7ux42 rhodospirell
9	48	53.9	1916	2 Q6SLA5	Q6SLA5 gibberella
10	47	52.8	148	2 Q6ZB15	Q6ZB15 oryza sativ
11	47	52.8	2936	2 Q7YRK8	Q7YRK8 canis famil
12	46	51.7	181	2 Q9TRZ5	Q9TRZ5 oryctolagus
13	46	51.7	231	2 Q69LM3	Q69LM3 oryza sativ
14	46	51.7	605	2 Q62F10	Q62F10 burkholderi
15	46	51.7	605	2 Q63VC3	Q63VC3 burkholderi
16	46	51.7	729	1 COA1_PAVP9	P33484 porcine par
17	46	51.7	729	1 COA1_PAVPK	P52501 porcine par
18	46	51.7	729	1 COA1_PAVPN	P18546 porcine par
19	46	51.7	729	2 Q6PS59	Q6PS59 porcine par
20	46	51.7	729	2 Q6TDP7	Q6TDP7 porcine par
21	45	50.6	111	2 Q87DB2	Q87DB2 xylella fas
22	45	50.6	117	2 Q623N2	Q623N2 oryza sativ
23	45	50.6	136	2 Q6BQS4	Q6BQS4 debaryomyce
24	45	50.6	149	2 Q69IV1	Q69IV1 oryza sativ
25	45	50.6	166	2 Q6DUM1	Q6DUM1 oryza sativ
26	45	50.6	178	2 Q7XY38	Q7XY38 griffithsia
27	45	50.6	326	2 Q7U8Z9	Q7U8Z9 synechococc
28	45	50.6	352	2 Q9LI15	Q9LI15 oryza sativ
29	45	50.6	476	2 Q6FYA2	Q6FYA2 candida gla
30	45	50.6	517	2 Q66CS9	Q66CS9 yersinia ps
31	45	50.6	517	2 Q8ZGK0	Q8ZGK0 yersinia pe

32	45	50.6	523	2	Q74VK5	Q74vk5 yersinia pe
33	45	50.6	548	2	Q76EM4	Q76em4 gluconobact
34	45	50.6	689	1	CA29_HUMAN	Q14055 homo sapien
35	45	50.6	802	2	Q6UX38	Q6ux38 homo sapien
36	45	50.6	802	2	Q7LFU5	Q7lfu5 homo sapien
37	45	50.6	802	2	Q86XS2	Q86xs2 homo sapien
38	45	50.6	883	2	Q9Y2J5	Q9y2j5 homo sapien
39	45	50.6	1294	2	Q9S814	Q9s814 arabidopsis
40	45	50.6	1687	2	Q8T9L7	Q8t9l7 toxoplasma
41	44.5	50.0	379	2	Q67TH2	Q67th2 symbiobacte
42	44.5	50.0	545	1	YB90_YEAST	P38346 saccharomyc
43	44.5	50.0	625	2	Q8L4G8	Q8l4g8 oryza sativ
44	44	49.4	128	2	Q93JD6	Q93jd6 streptomyce
45	44	49.4	152	2	Q6YWK9	Q6ywk9 oryza sativ

ALIGNMENTS

RESULT 1

ID	FGFL_HUMAN	STANDARD;	PRT;	209 AA.
AC	Q9NSA1:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).			
GN	Name=FGF21;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20461777; PubMed=10858549; DOI=10.1016/S0167-4781(00)00067-1;			
RA	Nishimura T., Nakatake Y., Konishi M., Itoh N.;			
RT	"Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";			
RL	Biochim. Biophys. Acta 1492:203-206(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bruen J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[3]			
RP	SEQUENCE OF 29-43.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";			
RL	Protein Sci. 13:2819-2824(2004).			
CC	-!- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-!- SIMILARITY: Belongs to the heparin-binding growth factors family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

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DR EMBL; AB021975; BAA99415.1; -.
DR EMBL; AY359086; AAO89444.1; -.
DR HSSP; P03968; 1BAR.
DR Genew; HGNC:3678; FGF21.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1_HBGF.
DR PRINTS; PR000831; IL1_HBGF.
DR PROSITE; PS00247; HBGF_FGF; FALSE NEG.
KW Direct protein sequencing; Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 209 Fibroblast growth factor-21.
FT CONFLICT 23 23 Missing (in Ref. 2).
FT DISSCRIPT 23 23
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 145 HLPGNKSPHRDPAPR 159

RESULT 2
Q8N683 PRELIMINARY; PRT; 209 AA.
ID Q8N683
AC Q8N683
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 21,.
GN Name=FGF21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.J., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
DR EMBL; BC018404; AAH18404.1; -.
DR HSSP; O95750; 1PWA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGF_FGF.
DR PRINTS; PR00262; IL1_HBGF.
DR PRINTS; PD000831; IL1_HBGF.
DR PRODOM; PD000831; IL1_HBGF.
DR SMART; SM00442; FGF; 1.
KW Growth factor.
SQ SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;

Query Match 100.0%; Score 89; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 145 HLPGNKSPHRDPAPR 159

RESULT 3
Q63624 PRELIMINARY; PRT; 1173 AA.
ID Q63624
AC Q63624
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=96293459; PubMed=8692929; DOI=10.1073/pnas.93.14.6975;
RA Yuryev A., Patturajan M., Litingtung Y., Joshi R.V., Gentile C.,
RA Gebara M., Corden J.L.;
RT "The C-terminal domain of the largest subunit of RNA polymerase II
interacts with a novel set of serine/arginine-rich proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 93:6975-6980(1996).
DR EMBL; U49056; AAC52657.1; -.
DR PIR; T31421; T31421.
SQ SEQUENCE 1173 AA; 124774 MW; 2F5209A6435F6770 CRC64;

Query Match 58.4%; Score 52; DB 2; Length 1173;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPA 14
DB 224 PGDPSPHREPP 235

RESULT 4
Q9YC35 PRELIMINARY; PRT; 165 AA.
ID Q9YC35
AC Q9YC35
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein APE1416.
GN OrderedLocusNames=APE1416;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OC NCBI_TaxID=56636;
RN [1]_TaxID=56636;
RP SEQUENCE FROM N.A.

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RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000061; BAA80413.1; -.
DR PIR; G72619; G72619.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 165 AA; 18858 MW; D73D0855F4D7A378 CRC64;

Query Match 56.2%; Score 50; DB 2; Length 165;
Best Local Similarity 68.8%; Pred. No. 16;
Matches 11; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 2 LPGNK--SPHRDPAPR 15
Db 140 LPANSGSPHRDPAPR 155

RESULT 5
Q9SSY2
ID Q9SSY2 PRELIMINARY; PRT; 355 AA.
AC Q9SSY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aux/IAA protein.
GN Name=CsiAA2;
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20267442; PubMed=10809445; DOI=10.1023/A:1006379804678;
RA Fujii N., Kamada M., Yamasaki S., Takahashi H.;
RA "Differential accumulation of Aux/IAA mRNA during seedling development
RT and gravity response in cucumber (Cucumis sativus L.).";
RL Plant Mol. Biol. 42:731-740(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22149308; PubMed=12151412;
RA Mizuno H., Kobayashi A., Fujii N., Yamashita M., Takahashi H.;
RT "Hydrostatic response and expression pattern of auxin-inducible gene,
RT CS-IAA1, in the primary roots of clinorotated cucumber seedlings.";
RL Plant Cell Physiol. 43:793-801(2002).
DR EMBL; AB026822; BAA5821.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046983; F:protein dimerization activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR GO; GO:0006445; P:regulation of translation; IEA.
DR InterPro; IPR011525; AUXIAA_ARF_dimer.
DR InterPro; IPR003311; AUX_IAA.
DR Pfam; PF02309; AUX_IAA; 1.
DR PROSITE; PS09962; IAA_ARF; 1.
SQ SEQUENCE 355 AA; 39030 MW; C471B7622522BBD8 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 355;
Best Local Similarity 72.7%; Pred. No. 71;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDP 12
Db 78 LPGSESPRDP 88

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RESULT 6
Q9WXX1
ID Q9WXX1 PRELIMINARY; PRT; 492 AA.
AC Q9WXX1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sugar kinase, FGGY family.
GN OrderedLocusNames=TM0116;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 393:323-329(1999).
CC -1- SIMILARITY: Belongs to the fucokinase / gluconokinase /
CC glycerokinase / xylokinase family.
DR EMBL; AE001697; AAD35210.1; -.
DR PIR; C72417; C72417.
DR TIGR; TM0116; -.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0004856; P:xylokinase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005957; P:xylose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR001448; SASP.
DR InterPro; IPR006000; Xylulokinase.
DR Pfam; PF02782; FGGY_C; 1.
DR Pfam; PF00370; FGGY_N; 1.
DR TIGRfams; TIGR01312; XylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
DR PROSITE; PS00304; SASP_1; UNKNOWN_1.
DR Complete proteome; Kinase; Transferase.
SQ SEQUENCE 492 AA; 54405 MW; 0F66A3AB451D88E1 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 492;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 340 YLNGERTPHRDPAPR 354

RESULT 7
Q9BLT0
ID Q9BLT0 PRELIMINARY; PRT; 574 AA.
AC Q9BLT0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Possible monocarboxylate transporter protein.
GN Name=L6071.01;
OS Leishmania major.
OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RX Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,

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RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:133-145(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL583933; CAC32260.1; -.
 DR InterPro; IPR006105; Try/amy1 inhib.
 DR PROSITE; PS00426; CEREAL TRYP AMYL INH; UNKNOWN 1.
 SQ SEQUENCE 574 AA; 61489 MW; C22D8283F06965E CRC64;

Query Match 53.9%; Score 48; DB 2; Length 574;
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLPKNSPHRD PAP 14
 DB 219 HARGNSPAREPSP 232

RESULT 8
 SYQ_RHOBA STANDARD; PRT; 601 AA.
 AC Q7UX42;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.18) (Glutamine-tRNA ligase) (GlnRS).
 DE (GlnRS).
 GN Name=glnS; OrderedLocusNames=RB1578;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 RL CC -!- CATALYTIC ACTIVITY: ATP + L-glutamine + tRNA(Gln) = AMP + diphosphate + L-glutamyl-tRNA(Gln).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; BX294135; CAD72170.1; -.
 DR HAMAP; MF_00126; -; 1.
 DR InterPro; IPR004514; GlnS.
 DR InterPro; IPR000924; Glu tRNA-synt_1c.
 DR Pfam; PF00749; tRNA-synt_1c; 1.
 DR Pfam; PF03950; tRNA-synt_1c.C; 1.
 DR TIGRFAMs; TIGR00440; glnS; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
 KW Protein biosynthesis.
 FT SITE 76 86 "HIGH" region.
 FT SITE 308 312 "KMSKS" region.

FT BINDING 311 311 ATP (By similarity).
 SQ SEQUENCE 601 AA; 68668 MW; 0C6B526811FF4CD3 CRC64;

Query Match 53.9%; Score 48; DB 1; Length 601;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14
 DB 181 PGNKSPHRDRTP 192

RESULT 9
 Q6SLA5 PRELIMINARY; PRT; 1916 AA.
 ID Q6SLA5
 AC Q6SLA5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative response regulator receiver RIM15p.
 GN Name=RIM15;
 OS Gibberella moniliformis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=117187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 38932;
 RX PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
 RA Catlett N.L., Yoder O.C., Turgeon B.G.;
 RT "Whole-genome analysis of two-component signal transduction genes in fungal pathogens.";
 RT Eukaryotic Cell 2:1151-1161(2003).
 RL CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AY456045; AAR30133.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0000150; P:two-component signal transduction system (p. . .); IEA.
 DR InterPro; IPR011006; CheY-like.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000014; PAS.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000408; Reg_Chrcondens.
 DR InterPro; IPR003789; Response_reg.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 2.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00091; PAS; 1.
 DR SMART; SM00448; REC; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00219; TyrK; 1.
 DR PROSITE; PS01112; PAS; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00626; RCC1_2; UNKNOWN 1.
 DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 DR ATP-binding; Kinase; Phosphorylation; Sensory transduction;
 KW Serine/threonine-protein kinase; Transferrase;
 SQ SEQUENCE 1916 AA; 209897 MW; 012264C6622FEADD CRC64;

Query Match 53.9%; Score 48; DB 2; Length 1916;
 Best Local Similarity 61.5%; Pred. No. 4.2e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 14
DB 623 LPNKTSPHRQESP 635

RESULT 10

Q62B15 PRELIMINARY; PRT; 148 AA.
AC Q62B15; (Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein OJ1449_H02.14;
GN Name=OJ1449_H02.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; AP004649; BAD01284.1; -;
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 15661 MW; 8D8023856854C02C CRC64;

Query Match 52.8%; Score 47; DB 2; Length 148;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 14
DB 82 LPANASPHHPLP 94

RESULT 11

Q7YRK8 PRELIMINARY; PRT; 2936 AA.
AC Q7YRK8; (Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Type VII collagen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22756273; PubMed=12874109; DOI=10.1093/hmg/ddg200;
RA Baldeschi C., Gache Y., Rattenholl A., Bouille P., Danos O.,
RT "Genetic correction of canine dystrophic epidermolysis bullosa mediated by retroviral vectors."
RL Hum. Mol. Genet. 12:1897-1905(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY163408; AA064414.1; -;
DR HSSP; P00981; IDTK.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; C1g helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR InterPro; IPR002035; WVF_A.
DR Pfam; PF01391; Collagen; 26.
DR Pfam; PF00041; fn3; 9.
DR Pfam; PF00014; Kunitz_BPTI; 1.

DR Pfam; PF00092; VWA; 2.
DR ProDom; PD000007; C1g_helix; 10.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00060; FN3; 9.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50853; FN3; 9.
DR PROSITE; PS50234; WVFA; 2.
KW Collagen.
SQ SEQUENCE 2936 AA; 293983 MW; F80CAF40E1F699B9 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 2936;
Best Local Similarity 57.1%; Pred. No. 9.3e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 15
DB 1372 LPGRGPGLDGPR 1385

RESULT 12

Q9TRZ5 PRELIMINARY; PRT; 181 AA.
AC Q9TRZ5; (Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 0(6)-methylguanine-DNA methyltransferase (EC 2.1.1.63).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181606; PubMed=8601571;
RA Sekiguchi M., Nakabeppu Y., Sakumi K., Tuzuki T.;
RT "DNA-repair methyltransferase as a molecular device for preventing mutation and cancer."
RL J. Cancer Res. Clin. Oncol. 122:199-206(1996).
DR HSSP; P16455; 1EH6.
DR GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR008332; MethylG_mtfase.
DR InterPro; IPR001497; Methyltransf_1.
DR Pfam; PF01035; Methyltransf_1; 1.
DR Pfam; PF02870; Methyltransf_1N; 1.
DR TIGRFAMs; TIGR00589; Ogt; 1.
DR PROSITE; PS00374; MGMT; 1.
SQ SEQUENCE 181 AA; 19397 MW; 12DF60974AAA1A16 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 181;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 13
DB 33 LPGKKTPEADPA 44

RESULT 13

Q69LM3 PRELIMINARY; PRT; 231 AA.
AC Q69LM3; (Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein B1136D08.121.
GN Name=B1136D08.121;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.

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OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu J., Yamagata H., Hayashi-Tugane M., Hijishita S., Fujisawa M.,
RA Shibata M., Itoh Y., Nakamura M., Sakaguchi M., Yoshihara R.,
RA Kobayashi H., Itoh K., Karasawa W., Yamamoto T., Saji S., Katagiri S.,
RA Kanamori H., Namiki N., Katayose Y., Matsumoto T., Sasaki T.,
RT "Composition and Structure of the Centromeric Region of Rice
RT Chromosome 8.";
RL Plant Cell 16:967-976 (2004).
DR EMBL; AP005832; BAD31755.1; -.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 25351 MW; 115DF2A67761B31C CRC64;

Query Match 51.7%; Score 46; DB 2; Length 231;
Best Local Similarity 61.5%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PGKNSPHRDPAPR 15
Db 103 PPSAQPHRDSAPR 115

RESULT 14
Q62F10
ID Q62F10 PRELIMINARY; PRT; 605 AA.
AC Q62F10;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Nitrite/sulfite reductase family protein.
GN ORFNames=BWA3052;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dmitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarrisa S.,
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL; CP000010; AAU48459.1; -.
SQ SEQUENCE 605 AA; 67257 MW; AC10A746FD4E7A89 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 605;
Best Local Similarity 64.3%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDPAPR 15
Db 361 LERNVAPHRDPARR 374

RESULT 15
Q63VC3
ID Q63VC3 PRELIMINARY; PRT; 605 AA.
AC Q63VC3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative nitrite/sulfite reductase.
GN ORFNames=BPSL1319;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songsivilai S., Stevens K., Tumapa S., Vesaratchaveh M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571965; CAH35316.1; -.
SQ SEQUENCE 605 AA; 67181 MW; 4F38B0B6EA3423AD CRC64;

Query Match 51.7%; Score 46; DB 2; Length 605;
Best Local Similarity 64.3%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDPAPR 15
Db 361 LERNVAPHRDPARR 374

Search completed: July 8, 2005, 22:18:07
Job time : 21.0625 secs

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